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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:28:36 ; Search time 70 Seconds

(without alignments)
565.363 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAAA.....LRGMGAFVLVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

1: /A_Geneseq_101002.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1553	100.0	297 21	AAU71031 Human adenine nucl
2	1553	100.0	297 22	AAU01198 Human adenine nucl
3	1553	100.0	297 23	AAU01378 Human adenine nucl
4	1457.5	93.9	298 19	AAU61169 Ant1 protein. Mus
5	1391.5	89.6	298 21	AAU71032 Human adenine nucl
6	1391.5	89.6	298 22	AAU01199 Human adenine nucl
7	1391.5	89.6	298 23	AAU01379 Human adenine nucl
8	1385.5	89.2	298 21	AAU71033 Human adenine nucl
9	1385.5	89.2	298 22	AAU39641 Human polypeptide
10	1385.5	89.2	298 22	AAU01200 Human adenine nucl

11	1385.5	89.2	298	23	AAU10380
12	1385.5	89.2	323	22	AAU41427
13	1294.5	83.4	325	22	ABG15423
14	1241	79.9	299	22	ABG66082
15	1241	79.9	299	22	ABG67300
16	1221.5	78.7	263	22	ABG27056
17	1147	73.9	307	22	ABG58380
18	1101.5	70.9	315	23	AAE21175
19	926.5	59.7	228	23	ABP43205
20	820	52.8	298	22	ABG18922
21	746	48.0	346	21	ACG36577
22	746	48.0	346	21	ACG37261
23	746	48.0	346	21	ACG37264
24	746	48.0	346	21	ACG38460
25	746	48.0	363	21	ACG36576
26	746	48.0	363	21	ACG37260
27	746	48.0	363	21	ACG37263
28	746	48.0	363	21	ACG38459
29	746	48.0	381	21	ACG36575
30	746	48.0	381	21	ACG37259
31	746	48.0	381	21	ACG37262
32	746	48.0	381	21	ACG38458
33	746	48.0	992	21	ACG38672
34	746	48.0	1009	21	ACG38671
35	746	48.0	1027	21	ACG38670
36	743	47.8	346	21	ACG17731
37	743	47.8	363	21	ACG17730
38	743	47.8	381	21	ACG17729
39	734	47.3	386	21	AAU00106
40	724.5	46.7	484	22	ABG15422
41	724.5	46.7	484	22	ABG17055
42	686	44.2	333	21	ACG06887
43	686	44.2	350	21	ACG06886
44	686	44.2	368	21	ACG06885
45	682	43.9	330	21	ACG20658

ALIGNMENTS

RESULT 1	ID	AAU71031	standard; Protein: 297 AA.
XX	XX	AAU71031:	
AC	AC		
XX	XX		
DT	DT	29-AUG-2000 (first entry)	
XX	XX		
DE	DE	Human adenine nucleotide translocator ANTI.	
XX	XX		
KW	KW	Human: adenine nucleotide translocator: ANTI; mitochondria: ADP: ATP;	
KW	KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;	
KW	KW	mitochondrial permeability transition; neuroprotective; neurotrophic;	
KW	KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	KW	antiparkinsonian; cerbroprotective; therapeutic; Huntington's disease; dystonia;	
KW	KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW	KW	diabetes; Leber's hereditary optic neuropathy; lactic acidosis; stroke; MIDD;	
KW	KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW	KW	myoclonic epilepsy red ragged fibre syndrome.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	WO200026370-A2.	
XX	XX		
PD	PD	11-MAY-2000.	
XX	XX		
PR	PR	03-NOV-1999; 99WO-US25883.	
XX	XX		
PR	PR	03-NOV-1998; 98US-0185904.	
PR	PR	08-SEP-1999; 99US-0393441.	
XX	XX		
PA	PA	(MITO-) MITOKOR.	

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR:
PI Ghosh SS:
DR WPI: 2000-365619/31.
DR N-PSDB: AAD00519.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
PS Claim 44: Page 172; 175pp; English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MEAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator [ANT] from human brain.
XX
SQ Sequence 297 AA:
Query Match 100.0%; Score 1553; DB 21; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVHASKOISAEKQYKGIIDCVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVHASKOISAEKQYKGIIDCVR 60
QY 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
DB 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
DB 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
QY 181 OGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFTVRRRMQ 240
DB 181 OGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFTVRRRMQ 240
QY 241 SGRKGADIMYGTGVCWKRIAKDEGAKAFKGAWSNVLRGCGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYGTGVCWKRIAKDEGAKAFKGAWSNVLRGCGAFVLVLYDEIKKYV 297

RESULT 2
AAU01198
ID AAU01198 standard: Protein: 297 AA.
XX
AC AAU01198:
XX
DT 07-SEP-2001 (first entry)
XX
DE Human adenine nucleotide translocator-1 (ANT-1) protein.
XX
KW Human: adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder: cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX

OS Homo sapiens.
XX
PN WO200132876-A2.
XX
XX 10-MAY-2001.
PD
XX
PT 03-NOV-2000; 2000MO-US30535.
XX
PR 03-NOV-1999; 99US-0434354.
XX
PA (MITO-) MITOKOR.
PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
PI Vellicelebi G, Davis RE:
XX
DR WPI: 2001-291054/30.
DR N-PSDB: AAS05901.
XX
PT New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure: Fig 2; 186pp; English.
XX
CC The present sequence represents human adenine nucleotide translocator-1
CC (ANT-1) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 297 AA:
Query Match 100.0%; Score 1553; DB 22; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVHASKOISAEKQYKGIIDCVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVHASKOISAEKQYKGIIDCVR 60
QY 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
DB 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
DB 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
QY 181 OGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFTVRRRMQ 240
DB 181 OGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFTVRRRMQ 240
QY 241 SGRKGADIMYGTGVCWKRIAKDEGAKAFKGAWSNVLRGCGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYGTGVCWKRIAKDEGAKAFKGAWSNVLRGCGAFVLVLYDEIKKYV 297

RESULT 3

AAU10378
 ID AAU10378 standard; Protein: 297 AA.
 XX
 AC AAU10378:
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 1 (ANT1).
 XX
 KW Human: adenine nucleotide translocator; ANT;
 KW mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200185944-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 11-MAY-2001; 2001WO-US15416.
 XX
 PR 11-MAY-2000; 2000US-0569327.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Cleverger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 DR N-PSDB: AAS16688.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide
 XX
 PS Claim 44: Fig 2: 147pp: English.
 XX
 CC The invention relates to a recombinant expression construct (1)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (1) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT1.
 XX
 SO Sequence 297 AA:
 Query Match 100.0%; Score 1553; DB 23; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.2e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MGDHWSFLKDFLAGAANAASKTAAPTEIEVKLLLOVOHASKOISAEKQYKGIIDCVR 60
 DB 1 MGDHWSFLKDFLAGAANAASKTAAPTEIEVKLLLOVOHASKOISAEKQYKGIIDCVR 60
 OY 61 IPKEGFLSPWRGNLANVIRPTQALNFAFKDKYKOLFGLGVDRHOFMYFGNLSG 120
 DB 61 IPKEGFLSPWRGNLANVIRPTQALNFAFKDKYKOLFGLGVDRHOFMYFGNLSG 120
 OY 121 GAAGATSLCFVYPLDFAATRIADVGRRAQREFHGLGDCIIRKFSKDSGLRGLYOGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFAATRIADVGRRAQREFHGLGDCIIRKFSKDSGLRGLYOGFNVSV 180
 OY 181 OGIIITRAAYFGVYDTAKGMLPDKNVHIFVSMIAOSVTAAGLLSTPPTVRRRMNQ 240

DB 181 OGIIITRAAYFGVYDTAKGMLPDKNVHIFVSMIAOSVTAAGLLSTPPTVRRRMNQ 240
 OY 241 SGRKADIMYTGTVDCRKRIAKDEGAKAFKGAANSNVLKMGCAFVLVLYDEIKKYV 297
 DB 241 SGRKADIMYTGTVDCRKRIAKDEGAKAFKGAANSNVLKMGCAFVLVLYDEIKKYV 297
 RESULT 4
 AAW61169
 ID AAW61169 standard; Protein: 298 AA.
 XX
 AC AAW61169;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Ant1 protein.
 XX
 KW ANT1. Adenine nucleotide translocator; cloning; screening;
 KW DNA tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;
 KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
 KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
 KW lactic acidosis; degenerative muscle disease.
 XX
 OS Mus sp.
 XX
 PN WO9819714-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 31-OCT-1997; 97WO-US19882.
 XX
 PR 01-NOV-1996; 96US-0030017.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Graham BC, Macgregor GR, Wallace DC;
 DR N-PSDB: AAV36479.
 XX
 PT Mice lacking heart-muscle adenine nucleotide translocator protein -
 PT useful as model for mitochondrial myopathy and hypertrophic
 PT cardiomyopathy in animals and to test therapeutic compositions or
 PT gene therapies
 XX
 PS Disclosure: Page 39-40; 61pp: English.
 XX
 CC The present sequence is the mouse Ant1 protein, the cDNA producing this
 CC polypeptide is cloned by screening a mouse heart cDNA library with the
 CC human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA
 CC Tag diodeoxy terminator cycle sequencing. The Ant1 protein is encoded by
 CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
 CC which can then be converted into ATP. An Ant1 homozygous mutant would
 CC thus be defective in OXPHOS which results in disease in oxidative
 CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
 CC used as a model system for fascioscapular humeral muscular dystrophy,
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
 CC independent of ANT1.
 XX
 SO Sequence 298 AA:
 Query Match 93.9%; Score 1457.5; DB 19; Length 298;
 Best Local Similarity 93.6%; Pred. No. 5e-162;
 Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
 OY 1 MGDHWSFLKDFLAGAANAASKTAAPTEIEVKLLLOVOHASKOISAEKQYKGIIDCVR 60
 DB 1 MGDHWSFLKDFLAGAANAASKTAAPTEIEVKLLLOVOHASKOISAEKQYKGIIDCVR 60

OY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFAPRTLRADVGR-RAOREFHGLGDCIIRKFSKDLRGLYOGFNNV 179
 DB 121 GAAGATSLCFVYPLDFAPRTLRADVGR-RAOREFHGLGDCIIRKFSKDLRGLYOGFNNV 180
 OY 180 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 239
 DB 181 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 240
 OY 240 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGMGAFVLLYDEIRKYYV 297
 DB 241 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGMGAFVLLYDEIRKYYV 298

RESULT 5
 ID AAY71032 standard; Protein: 298 AA.
 AAY71032:
 29-AUG-2000 (first entry)
 Human adenine nucleotide translocator ANT2.
 Human: adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nontropic; antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
 KM
 XX Homo sapiens.
 OS
 PN WO200026370-A2.
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99WO-US25883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS;
 DR N-PSDB; AAD00520.
 DR
 DR MPI: 2000-365619/31.
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 45; Page 172-173; 175pp; English.
 PS
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC d(ATP)-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated

CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX
 SO Sequence 298 AA:
 Query Match 89.6%; Score 1391.5; DB 21; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2,7e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 OY 1 MGDHAWFLKDLFLAGAAVAASVTAAPRIERVKLLLOVHASKQISAEKQYKIDCVNR 60
 DB 1 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 60
 OY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFAPRTLRADVGR-RAOREFHGLGDCIIRKFSKDLRGLYOGFNNV 179
 DB 121 GAAGATSLCFVYPLDFAPRTLRADVGR-RAOREFHGLGDCIIRKFSKDLRGLYOGFNNV 180
 OY 180 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 239
 DB 181 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 240
 OY 240 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGMGAFVLLYDEIRKYYV 296
 DB 241 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGMGAFVLLYDEIRKYYV 297

RESULT 6
 ID AAU01199 standard; Protein: 298 AA.
 AAU01199:
 07-SEP-2001 (first entry)
 Human adenine nucleotide translocator-2 (ANT-2) protein.
 Human: adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 PN WO200132876-A2.
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LC;
 PI Velicelabi G, Davis RE;
 DR N-PSDB; AAS05902.
 DR
 DR MPI: 2001-291054/30.
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX

PS Disclosure: Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

SO Sequence 298 AA:

Query Match 89.6%; Score 1391.5; DB 22; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.7e-154;
 Matches: 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGKGIIDCVR 60
 DB 1 MTDALSTFAKDFLAGAANAASKTAVAPIERVKLLQVOHASKOITADKOKGIIIDCVR 60

OY 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFMYRFAGNLNSG 120
 DB 61 IPKEEVLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFMYRFAGNLNSG 120

OY 121 GAAGATSLCFYVPLDFARTRLAADVGR-AOREFHGIDLCIYIKFSKGLGLVGGFNVS 179
 DB 121 GAAGATSLCFYVPLDFARTRLAADVGR-AOREFHGIDLCIYIKFSKGLGLVGGFNVS 180

OY 180 VOGIIYRAAFCGYVDTAAGMLPDPKNVHIFVSMIAOSVTAVAGLSYPPDYRRRMM 239
 DB 181 VOGIIYRAAFCGYVDTAAGMLPDPKNVHIFVSMIAOTVAVAGLSYPPDYRRRMM 240

OY 240 OSGRKGADIMYTGTCWKRKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 296
 DB 241 OSGRKGTDIMYTGTCWKRKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 297

RESULT 7
 AAU10379 standard; Protein: 298 AA.

AC AAU10379;
 DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 2 (ANT2).
 KW Human: adenine nucleotide translocator; ANT; ss;
 KW mitochondrial matrix protein.

OS Homo sapiens.
 PN WO200185944-A2.
 PD 15-NOV-2001.
 PF 11-MAY-2001; 2001WO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 PA (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
 XX WPI: 2002-055598/07.
 DR N-PSDB; AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide .

PS Claim 44: Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.

SO Sequence 298 AA:

Query Match 89.6%; Score 1391.5; DB 23; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.7e-154;
 Matches: 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGKGIIDCVR 60
 DB 1 MTDALSTFAKDFLAGAANAASKTAVAPIERVKLLQVOHASKOITADKOKGIIIDCVR 60

OY 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFMYRFAGNLNSG 120
 DB 61 IPKEEVLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFMYRFAGNLNSG 120

OY 121 GAAGATSLCFYVPLDFARTRLAADVGR-AOREFHGIDLCIYIKFSKGLGLVGGFNVS 179
 DB 121 GAAGATSLCFYVPLDFARTRLAADVGR-AOREFHGIDLCIYIKFSKGLGLVGGFNVS 180

OY 180 VOGIIYRAAFCGYVDTAAGMLPDPKNVHIFVSMIAOSVTAVAGLSYPPDYRRRMM 239
 DB 181 VOGIIYRAAFCGYVDTAAGMLPDPKNVHIFVSMIAOTVAVAGLSYPPDYRRRMM 240

OY 240 OSGRKGADIMYTGTCWKRKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 296
 DB 241 OSGRKGTDIMYTGTCWKRKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 297

RESULT 8
 AAU1033 standard; Protein: 298 AA.

AC AAU1033;
 DT 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANT3.
 KW Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotropic;
 KW antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuropletic;
 KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;

KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 OS Homo sapiens.
 XX
 XX
 PN WO200026370-A2.
 PD 11-MAY-2000.
 XX
 XX
 PF 03-NOV-1999: 99MO-US25883.
 XX
 XX
 PR 03-NOV-1998: 98US-0185904.
 PR 08-SEP-1999: 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 P1 Ghosh SS.
 DE WPI: 2000-365619/31.
 DE N-PSDB: AAD00521.
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 XX against mitochondrial disease
 XX
 PS Claim 46, Page 173-174; 175pp; English.
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC d/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia.
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 XX
 XX
 SQ Sequence 298 AA:
 Query Match 89.2%; Score 1385.5; DB 21: Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.4e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 Oy 1 MGDHANSFLKDFLAGVAAAVSTAAPIERVKLLQOVHASKOISAEKOYKIIDCVVR 60
 Db 1 MPEQATISFAKDFLAGGIAAIAAKSTAAPIERVKLLQOVHASKOIAADKOYKIVDCIYV 60
 Oy 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKKYKOLFSGVDKHTQFRRFAGMLASG 120
 Db 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKKYKOLFSGVDKHTQFRRFAGMLASG 120
 Oy 121 GAAGATSLCFVPLDFARTRLADVGR-AQREFHGLGCIIRIFPSDGLRGLYQSPNVS 179
 Db 121 GAAGATSLCFVPLDFARTRLADVGRSGTEREFRLGDCIVVITTSDDGLRGLYQSPNVS 180
 Oy 180 VOCIITTYRAAYFCVYDTAFKAGLMDPKNNVHIFVSWMTAQSVAVALSTPFDTVRRMM 239
 Db 181 VOCIITTYRAAYFCVYDTAFKAGLMDPKNNVHIFVSWMTAQSVAVALSTPFDTVRRMM 240
 Oy 240 OSGRKGADIMYTCTVDCMKRIFKDEGKAFKFGKANSNVLKMGCAFVLVLYDELRKYV 297
 Db 240 OSGRKGADIMYTCTVDCMKRIFKDEGKAFKFGKANSNVLKMGCAFVLVLYDELRKYV 297

Db 241 OSGRKGADIMYTCTVDCMKRIFKDEGKAFKFGKANSNVLKMGCAFVLVLYDELRKYV 298
 RESULT 9
 AAM39641
 ID AAM39641 standard; Protein: 298 AA.
 XX
 XX
 AC AAM39641:
 XX
 XX
 DT 22-OCT-2001 (first entry)
 XX
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 XX
 KM Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KM leukaemia.
 XX
 XX
 OS Homo sapiens.
 OS
 PN WO200153312-A1.
 XX
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;
 XX
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AA158797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 XX
 PS Example 4: SEQ ID NO 2786; 10078pp; English.
 XX
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM39642-AAM42213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Actin/inhibin activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 XX
 SQ Sequence 298 AA:
 Query Match 89.2%; Score 1385.5; DB 22: Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.4e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 Oy 1 MGDHANSFLKDFLAGVAAAVSTAAPIERVKLLQOVHASKOISAEKOYKIIDCVVR 60
 Db 1 MPEQATISFAKDFLAGGIAAIAAKSTAAPIERVKLLQOVHASKOIAADKOYKIVDCIYV 60
 Oy 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKKYKOLFSGVDKHTQFRRFAGMLASG 120
 Db 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKKYKOLFSGVDKHTQFRRFAGMLASG 120
 Oy 121 GAAGATSLCFVPLDFARTRLADVGR-AQREFHGLGCIIRIFPSDGLRGLYQSPNVS 179
 Db 121 GAAGATSLCFVPLDFARTRLADVGRSGTEREFRLGDCIVVITTSDDGLRGLYQSPNVS 180
 Oy 180 VOCIITTYRAAYFCVYDTAFKAGLMDPKNNVHIFVSWMTAQSVAVALSTPFDTVRRMM 239
 Db 181 VOCIITTYRAAYFCVYDTAFKAGLMDPKNNVHIFVSWMTAQSVAVALSTPFDTVRRMM 240
 Oy 240 OSGRKGADIMYTCTVDCMKRIFKDEGKAFKFGKANSNVLKMGCAFVLVLYDELRKYV 297
 Db 240 OSGRKGADIMYTCTVDCMKRIFKDEGKAFKFGKANSNVLKMGCAFVLVLYDELRKYV 297

CC The invention relates to a recombinant expression construct (1)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
CC ANT polypeptide by transfecting a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (1) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT3.
XX
S0 Sequence 298 AA:

Query Match 89.2%: Score 1385.5; DB 23; Length 298;
Best Local Similarity 87.2%: Pred. No. 1.4e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHWSFLKDFLAGNAVAASKTVAPIERVKLLLOVHASKOISAEKOYKGIIDCVR 60
DB 1 MTEQALSFADFLAGGIAAAISKTAAPIERVKLLLOVHASKOIAADKOYKGIIDCVR 60
OY 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKDYKOLFLGVDRIHQFMRYPFAGNLASG 120
DB 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKDYKOLFLGVDRIHQFMRYPFAGNLASG 120
OY 121 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIRKFSQGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIRKFSQGLRGLYOGFNV 180
OY 180 VOGIIRYRAAYFCGYVDPAKGMPLDPKKNVHIFVSMMAIOSYTAAGLLSTPFDVRRRM 239
DB 181 VOGIIRYRAAYFCGYVDPAKGMPLDPKKNVHIFVSMMAIOSYTAAGLLSTPFDVRRRM 240
OY 240 QSGRKADIMYGTGTCVDCWKRIRAKDEGAKAFKAGMSNVLRGMCAPVLYLYDEIKKYV 297
DB 241 QSGRKADIMYGTGTCVDCWKRIRAKDEGAKAFKAGMSNVLRGMCAPVLYLYDEIKKYV 298

RESULT 12
AAM41427 ID AAM41427 standard; Protein: 323 AA.
XX
AC AAM41427:
XX
DT 22-OCT-2001 (first entry)
DE
XX Human polypeptide SEQ ID NO 6358.
XX
KM Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
KM leukemia.
OS Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX
XX 25-APR-2000; 2000US-0552317.
XX
XX 09-JUL-2000; 2000US-0598042.
XX

PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB: AA160383.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries.
XX
PS Example 2: SEQ ID NO 6358; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nocotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
S0 Sequence 323 AA:

Query Match 89.2%: Score 1385.5; DB 22; Length 323;
Best Local Similarity 87.2%: Pred. No. 1.6e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHWSFLKDFLAGNAVAASKTVAPIERVKLLLOVHASKOISAEKOYKGIIDCVR 60
DB 26 MTEQALSFADFLAGGIAAAISKTAAPIERVKLLLOVHASKOIAADKOYKGIIDCVR 85
OY 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKDYKOLFLGVDRIHQFMRYPFAGNLASG 120
DB 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKDYKOLFLGVDRIHQFMRYPFAGNLASG 145
OY 86 IPKEGFLSFMRGNLANVIRYPTQALNFAFKDYKOLFLGVDRIHQFMRYPFAGNLASG 179
DB 121 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIRKFSQGLRGLYOGFNV 205
OY 146 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIRKFSQGLRGLYOGFNV 239
DB 180 VOGIIRYRAAYFCGYVDPAKGMPLDPKKNVHIFVSMMAIOSYTAAGLLSTPFDVRRRM 265
OY 206 VOGIIRYRAAYFCGYVDPAKGMPLDPKKNVHIFVSMMAIOSYTAAGLLSTPFDVRRRM 297
DB 240 QSGRKADIMYGTGTCVDCWKRIRAKDEGAKAFKAGMSNVLRGMCAPVLYLYDEIKKYV 323
OY 266 QSGRKADIMYGTGTCVDCWKRIRAKDEGAKAFKAGMSNVLRGMCAPVLYLYDEIKKYV 323

RESULT 13
ABG15423 ID ABG15423 standard; Protein: 325 AA.
XX
XX ABG15423:
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #15414.
DE

[illegible]

Oy		237	MMNOSGRGADIMYGTATDCWPKIAKDEGAKAFPGAMSNVLRMGCAFVLVXD-EIKK	295
Dd		264	EXMOSRGKTDMYTGLTDCWKIARDEGKAFFKGAMSNVLRMGCAFVLVYEKKSKK	323
Oy		296 Y 296 		
Dd		324 Y 324		
		RESULT 14		
		ID ABB66082		
		ABBB6082 standard; Protein: 299 AA.		
XX	AC	ABBB6082:		
XX	DT	26-MAR-2002 (first entry)		
XX	DE	Drosophila melanogaster polypeptide SEQ ID NO 25038.		
KX	KW	Drosophila: developmental biology; cell signalling; insecticide;		
XX	KW	pharmaceutical.		
XX	OS	Drosophila melanogaster.		
XX	PN	WO200171042-A2.		
XX	PD	27-SEP-2001.		
XX	PE	23-MAR-2001; 2001WO-US09231.		
PR	PR	23-MAR-2000; 2000US-191637P.		
XX	XX	11-JUL-2000; 2000US-0614150.		
PA		(PERE) PE CORP NY.		
PI		Venter JC, Adams M, Li PWD, Myers EW:		
DR		WP1: 2001-656860/75.		
XX	DR	N-PSDB: ABL10185.		
PT		New isolated nucleic acid detection reagent for detecting 1000 or more		
PT		genes from Drosophila and for elucidating cell signalling and cell-cell		
PT		interactions -		
PS		Disclosure: SEQ ID NO 25038; 21pp + Sequence Listing; English.		
CC		The invention relates to an isolated nucleic acid detection reagent		
CC		capable of detecting 1000 or more genes from Drosophila. The invention is		
CC		useful in developmental biology and in elucidating cell signalling and		
CC		cell-cell interactions in higher eukaryotes for the development of		
CC		insecticides, therapeutics and pharmaceutical drugs. The invention		
CC		discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA		
CC		sequences (ABL01840-ABL16175) and the encoded proteins		
CC		(ABB57737-ABB72072).		
CC		The sequence data for this patent did not form part of the printed		
CC		specification, but was obtained in electronic format directly from WIPO		
CC		at ftp.wipo.int/pub/published_pct_sequences.		
XX				
SQ		Sequence 299 AA:		
Oy		Query Match 79.9%; Score 1241; DB 22; Length 299;		
		Best Local Similarity 79.7%; Pred. No. 1,2e-136;		
		Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0		
Dd		5 AMSFLKDPLAGAVAAASKTVAPLIERVKLLLOVGHASHSNOISAEIOYKGIIDCVRIPRE 64		
		: : : :		
Oy		7 AVGEFKDDAAGGISAAVSASTAVAPIERVKLLLOVOHISKQISPDKOYKGMVCFFIRIPE 66		
Dd		65 OGFSEFMGNLANVIRFPTOLANFAFDKYKQLFGVDNRKHOFRRYPAGNIASGAAG 124		
Oy		67 OGSSFSFMGNLANVIRFPTOLANFAFDKYKQYLVGCYDKNRTORFRRYPAGNIASGAAG 126		
Oy		125 ATSLCEVVPDLDFARTRLADVGGRAOREFHGLGDICIIKFNSDGLRGLGYGFNVSVOGII 184		

D_b 127 ATSLCFVYPLDFAFRLTAADTGKGGGREFETGLGNCUTLRIKPSDGIYGLYRFGVSYGII 166

O_y 185 IYPAATFCVYDTAKGKLDPKKNVHIFVSMIAQSTAVAGLSTPDTVRRRRMMOSGRK 244

D_b 187 IYRAAFGFGYDTRGRLDPKKNPIYIISMAIQVYTTAAGIVSYPFDFVRRRRMMOSGRK 246

O_y 245 GAIIMTGTVDCAWRKIAKDEGAFAFFKGAQMSNVLLGMGAPFLVLYDEIKK 295

D_b 247 ATEVILIKNTLHCAATIAKQEGTGAFFKGAQMSNVLLMGTCGAPFLVLYDEIKK 297

RESULT 15
APR67200

ID ABB67300 standard; Protein; 299 AA.

AC ABB67300;

DT 26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 28692

KW *Drosophila*; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

05 *Drosophila melanogaster*.

PN WO200171042-

PD 27-SEP-2001

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P

XX

XX

XX
2007-06-09

DR N-PsDB; ABL11403.

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT interactions

PS Disclosure; SEQ ID NO 28692; 21pp + Sequence Listing; English

CC The invention relates to an isolated nucleic acid detection reagent

CC useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes.

CC Insecticides, therapeutics and pharmaceutical drugs. The invention

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABR57737-ABR72073)

CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in a laboratory of the University of

CC at ftp.wipo.int/published_pct_sequences

SQ Sequence 299 AA;

Query Match	79.98;	Score 1241;	DB 22;	Length 299
Post Local Client:	70.79;	Score 1241;	DB 22;	Length 299

Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;

QY 5 AWSFLKDFLAGAANAASKTAVAPIERVKLLLOVQHASKQISAEKOYKGIIDCVVRIPKE 64

Db 7 AVGFVKDFAAGCISAASVTAVAPIERVKLLQVQHISKQISPDKQYKGMVDCFIRIPKE 66

QY 65 OGFLSFWRCNLNVI RYPTQALNEAFKDKYKQLFLGGVDRHKQFWRYFAGNLSGGAAG 124

D6	6	QGFSSFWRCGLNAVIVYPTQALNFAFKDKYKQVEFLGVDNDNTQFMWRFAGNLASGGAA	136
Oy	125	ATSLCEVYPPLDFAFRTFLADVCRRAOREFHGIGDCI I I F S D G L R G L Y O G F P N V S V G I I	184
D6	127	ATSLCEVYPPLDFEAFRPLADDTCKGCGORETFTTG I I I I I I I I I I I I I I I I I I	186
Oy	185	IYBAAAFEGYDTRAKGLDPKKNVH I FVSMTI NOSVTAVAAGLSLYPFDTVRRRMMOSGRK	244
D6	187	IYBAAAFEGYDTRAKGLDPKKNTPIYISAI AOVVTVAAGIVSTPFDVRRRRMMOSGRK	246
Oy	245	GADIWTGYDWCWR I AKDECAKAFFPKGMSNVLRMGKGAEVLVYLDEIKK	295
D6	247	ATEYITKNLTHCMATTAKOEGCAFPPKCAFSLILGTSGAPLVLYLDEIKK	297

Search completed: June 18, 2003, 13:34:03
Job time : 71 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Fun on: June 18, 2003, 13:20:01 ; Search time 15 Seconds

(Without alignments)
582.574 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAAA.....LRGMGAFVLVDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents, AA: *
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep: *
7: /cgn2_6/ptodata/1/1aa/6D.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1457.5	93.9	298	3	US-08-961-871-10
2	301	19.4	469	4	US-09-188-930-339
3	291	18.7	447	4	US-09-160-119-4
4	291	18.7	674	4	US-09-160-119-2
5	267	17.2	291	4	US-09-501-558-2
6	238	15.3	320	2	US-08-933-750C-12
7	238	15.3	320	4	US-09-234-613-12
8	233.5	15.0	312	4	US-09-142-565-2
9	227	14.6	299	1	US-08-518-878B-56
10	227	14.6	299	2	US-08-470-868A-56
11	227	14.6	309	1	US-08-518-878B-51
12	227	14.6	309	2	US-08-807-861A-51
13	227	14.6	309	2	US-08-470-868A-51
14	227	14.6	309	3	US-09-210-681-51
15	227	14.6	309	3	US-08-946-719A-51
16	227	14.6	311	2	US-08-775-009-33
17	225	14.5	311	2	US-08-775-009-33
18	222.5	14.3	308	2	US-08-937-466-2
19	222.5	14.3	308	2	US-09-172-528-2
20	222.5	14.3	308	4	US-09-318-199-2
21	222.5	14.3	308	4	US-09-503-579-2
22	218.5	14.1	432	2	US-08-937-466-4
23	218.5	14.1	432	2	US-09-172-528-4
24	218.5	14.1	432	3	US-09-318-199-4
25	218.5	14.1	432	4	US-09-503-579-4
26	208.5	13.4	293	4	US-09-501-558-4
27	196.5	12.7	307	2	US-08-807-861A-56

28	196.5	12.7	307	3	US-09-210-681-56	Sequence 56, Appl
29	196.5	12.7	307	3	US-08-946-719A-56	Sequence 56, Appl
30	193	12.4	303	1	US-08-294-522B-36	Sequence 36, Appl
31	192	12.4	303	1	US-08-518-878B-37	Sequence 37, Appl
32	192	12.4	303	2	US-08-807-861A-37	Sequence 37, Appl
33	192	12.4	303	2	US-08-470-868A-37	Sequence 37, Appl
34	192	12.4	303	3	US-09-210-681-37	Sequence 37, Appl
35	192	12.4	303	3	US-08-946-719A-37	Sequence 37, Appl
36	190.5	12.3	306	5	PCT-US94-09799-1	Sequence 1, Appl
37	188.5	12.1	351	2	US-08-933-750C-19	Sequence 19, Appl
38	188.5	12.1	351	4	US-09-234-613-19	Sequence 19, Appl
39	185.5	11.9	328	4	US-09-068-140A-15	Sequence 15, Appl
40	176	11.3	256	2	US-08-937-466-6	Sequence 6, Appl
41	176	11.3	256	2	US-09-172-528-6	Sequence 6, Appl
42	176	11.3	256	3	US-09-318-199-6	Sequence 6, Appl
43	176	11.3	256	4	US-09-503-579-6	Sequence 6, Appl
44	176	11.3	312	4	US-09-188-930-142	Sequence 142, App
45	175.5	11.3	289	4	US-09-068-140A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
NUMBER OF INVENTION: Nucleotide Translocator Protein and Methods
CORRESPONDENCE ADDRESS: 11
ADDRESS: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 93.9%, Score 1457.5; DB 3; Length 298;
Best Local Similarity 93.6%; Pred. No. 4.1e-161;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
CY 1 MGDHMSFLKDFLAGAVAAVSKTRAVPIERVKLLLOVQASKQTSIAEKYKGIIDCVVR 60

```
|||||
Db 1 MDDQALSLFLKDLFLAGIAAASKTAVAPIERVKLLQVOHASKOISAEKQYGIITDCVVR 60
Oy 61 IPKEGGLFSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHKKOFWRYPAGNLASG 120
Db 61 IPKEGGLFSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHKKOFWRYPAGNLASG 120
Oy 121 GAAAGTSLCFVYPLDFARTTLAADVGKSSOREFNGLDCLTKIKSDGLKGLYOGFSVS 180
Db 121 GAAAGTSLCFVYPLDFARTTLAADVGKSSOREFNGLDCLTKIKSDGLKGLYOGFSVS 180
Oy 180 VOGIITIRAAVFGVYDTAKGMLPDPKNVHIIVSMIAOSVTAVAGLSPFTVRRRM 239
Db 180 VOGIITIRAAVFGVYDTAKGMLPDPKNVHIIVSMIAOSVTAVAGLSPFTVRRRM 239
Oy 240 OSGRGADIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGSGAFVLVYDEIKYV 297
Db 240 OSGRGADIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGSGAFVLVYDEIKYV 297
Oy 241 OSGRGADIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGSGAFVLVYDEIKYV 298
Db 241 OSGRGADIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGSGAFVLVYDEIKYV 298
```

RESULT 2

US-09-188-930-339
Sequence 339, Application US/09188930A
Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT FILING DATE: 1998-11-09
CURRENT APPLICATION NUMBER: US/09/188,930A
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-339

Query Match

Best Local Similarity 28.9%; Score 301; DB 4; Length 469;
Pred. No. 2,4e-26;

Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

```
Oy 6 WSFLKDFLAGAVAAVSKTAVAPIERVKLLQVOHASKOISAEKQYGIITDCVVR-R1 61
Db 187 WRLH--VAAGGAGAVSRCTAPLDRKLVLMQV-HASRSNM-----CLVGGFTOM 233
Oy 62 PKEGGLFSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDR-----HKOFWRYPAGN 116
Db 234 IREGGAKSLWRGNINVLKIAPEISAKIFMAYEQMKRLV--GSDQETLRHER----- 283
Oy 117 LASGGAAGTSLCFVYPLDFARTTLAADVGKSSOREFNGLDCLTKIKSDGLKGLYOGF 176
Db 284 LVAGSLAGIAOSSIVPMEVLKTRMAL---RKTGYSCMLDCARRLAKEGVAAAFYKGG 339
Oy 177 NVSGGIIIRAAVFGVYDTAKGMLPDPKNVHIIVSMIAOSVTAVAGLSPFTVRRRM 237
Db 340 IPMMLGIIIPYAGIDLAVETLKTWLOKRAVNSADP---GVFY-LLAGGISTTCOLAS 395
Oy 228 YPFDVRRRMMSOGRGADIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGSGAFV- 286
Db 396 YPLAVTRRMQAQASIEGAPEVTMSL--FKQILRTEGAGGLVRLAPNFMKVIYPAVSIS 453
Oy 287 LVLYDEIK 294
Db 454 YVYVENLK 461
```

RESULT 3

```
US-09-160-119-4
Sequence 4, Application US/09160119A
Patent No. 6316219
GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRILL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 447
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-160-119-4
```

Query Match

Best Local Similarity 18.7%; Score 291; DB 4; Length 447;
Pred. No. 3,2e-25;

Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

```
Oy 12 FLAGAVAAVSKTAVAPIERVKLLQVOHASKOISAEKQYGIITDCVVR1PKEGGLFSF 71
Db 104 FGLGSVAAGVATVAVPIDLVTRMQRNSTGCSFVGLYKNSFDFKFLVLRKEGFGLY 163
Oy 72 RGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHKKOFWRYPAGNLASGAGTSLCFV 131
Db 164 RGLLPDLGVAPPEAKKLTVDNPFVRKFM---HNDGSVPLAELIAGCAGGSOVIFT 218
Oy 132 YPLDFARTTL--AADV--GRRAREFHGDCI1KIFKSDGLKGLYOGFNVSGI11VR 187
Db 219 NPLEIVKIRLOVAGETTTGPRVS-----ALSVVRDLGFFGIYKKAACFLRBIIPS 269
Oy 188 AAYFGVYDTAKGMLPDPKNVHIIVSMIAOSVTAV-AGLSTPFTVRRRMMSOGRKGA 246
Db 270 AIFYPCYAHVHKASFANEDGVSPCSILLAGAIAGMPAASLVTPADVIKTR--LOVVARAG 327
Oy 247 DIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGSGAFVLVYDEIKY 296
Db 328 QTTYSGVIDCFRILREBGRKALMKGAGAVFRSSPQFGVTLTYELLDRW 378
```

RESULT 4
US-09-160-119-2
Sequence 2, Application US/09160119A
Patent No. 6316219
GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRILL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-160-119-2

Query Match

Best Local Similarity 18.7%; Score 291; DB 4; Length 674;

DB 243 RLQVGFHARAFAFGVRRYKGLMDCAKOVLOKEGALGFCKGLSPSLKALSTGFMFSS 302
OY 290 YD 291
DB 303 YE 304

RESULT 7
US-09-234-613-12
Sequence 12, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNOT02
CLONE: 207452
US-09-234-613-12

Query Match 15.3% Score 238 DB 4: Length 320:
Best Local Similarity 23.5% Pred. No. 2.8e-19;
Matches 71: Conservative 67; Mismatches 124; Indels 40; Gaps 10;

OY 13 LAGAVAAAVSKTAVAPIERVKLLLOVOHAS-KQISAEKQYKGIIDCVVRIPKEOGFLSFM 71
DB 20 VAGSVSGLVTRALISPFQVIXIRFQLOHERLSRSDPSAKYHIILOASROILOBEGPTAFW 79
OY 72 RGNLANVIRYPTQALNF-AFKDKYKQLFLGCVDRHKQFWRYPAGNLASGGAAGATSLCF 130
DB 80 KCHVPAQJLISIGYAVOFLSPFMTLTVHRSVYDAREFSVHF---VCGGLAACMATLTL 135
OY 131 VPLDPARTRLAADVGRARQREFHGLGDCIIKIFKSDGLRGLYGCFNNVSVGCIITIRAAV 190

DB 136 VHPVDVLRTRFAA---QGPVKYNTLRLHNAVGTMYSEGOVYTKGLAPLAIYFPYAGLO 192
OY 191 FGVYDTAKGMLDPPKKNVHIFVSMWI-----AQSVAAGCLLSYPPDTVVR 235
DB 193 FSCYSSLK-----ILLY-KMAIPAECKKNENJONLLCGSGAGVYISKTLTYPLDLFPK 242
OY 236 RMM---QSGRK--GADIMYTGCTVDCMKRIADDEGAKAFKCAKMSNVLR-GMGCAFVLVL 289
DB 243 RLQVGFHARAFAFGVRRYKGLMDCAKOVLOKEGALGFCKGLSPSLKALSTGFMFSS 302
OY 290 YD 291
DB 303 YE 304

RESULT 8
US-09-142-565-2
Sequence 2, Application US/09142565A
Patent No. 6187560
GENERAL INFORMATION:
APPLICANT: Lee James Beasley
APPLICANT: Kelly Paine
APPLICANT: Robert James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 312
TYPE: PRP
ORGANISM: HOMO SAPIEN
US-09-142-565-2

Query Match 15.0% Score 233.5 DB 4: Length 312:
Best Local Similarity 24.7% Pred. No. 9e-19;
Matches 73: Conservative 53; Mismatches 145; Indels 25; Gaps 8;

OY 12 FLAGAVAAAVSKTAVAPIERVKLLLOVOHASKQISAEK--QYKGIIDCVVRIPKEOGFLS 69
DB 17 FLAGATACGADLVLPFDITAKVRLQIOGENOAVOTARLVOTRGVLGITLVNRTREGPCS 76
OY 70 FWRGNLANVIRYPTQALNFAPFKDKYKQLFL-GVDRHKQFWRYPAGNLASGGAAGATSL 128
DB 77 PYNGLVAGIQRQMSFASIRIGLYDSVKQYTPKADNSLTFRILA-----CCTTGAMAV 131
OY 129 CFVYVLPDARTRLADV---GRRARREFGLDCLIKIFKSGGLGLVQGFNVSVQGIIT 185
DB 132 TCAOPTDVVKVRFQASIHLCPSRDSKYSCTMDAYRTIAREBGVGLKKGTLPIIMRAAI 191
OY 186 YRAAYFGVYDTAKGMLDPPKKNVHIFVSMWIAQSVTA-----VAGLSYPPDTVRRMMQ 240
DB 192 VVCAAEVYVYDILKEKLLD---YHLITDNFPCIFVSAFGCAFATVAVASVDVYVKTRYM-- 246
OY 241 SGRKGAIDIMYTGCTVDCMKRIADDEGAKAFKCAKMSNVLR-GMGCAFVLVLVDEIKK 295
DB 247 ---NSPPGOYFSPIDCMIKMVAQEGPTAFYKGFYTSFRLDSMNVNMFVTEQLKR 299

RESULT 9
US-08-518-878B-56
Sequence 56, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-51

Query Match 14.6% Score 227; DB 2; Length 309;
Best Local Similarity 23.8% Pred. NO. 5e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

Cy 12 FLAGVAAVSTAVAPIERVKLLLOVHASK---QISAEKQKGIIDCVIRPKEGFL 68
Db 17 FLAGCTAACIADLITFPDITAKVRLIOGESGPPVATVSAOYKGMGTILTWRTGPR 76
Cy 69 SFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDYDRHKQFWRYPAGNLASGAGATSL 128
Db 77 SLVNGLVAGLOROMSFASVRIGLYDSVKQFYTKGEHNS-----IGSRLASTGTALAV 131
Cy 129 CFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSDGLGLYOGFNVSOGIITIRA 188
Db 132 AVAOPTDVAKVFQOARAGCGRRYOSTVNAVKTIARECGFGLMKGTSPNARNAIVNC 191
Cy 189 AVFGYVDTRAK-----GMLPRPKNNHIFVSMHIAOSVYAVACLLSPEDTVRRMMQSG 242
Db 192 AELVYTDLIKDALLANLMTDLPCH-FTSAFGAGCTTV---IASPDVVVTRTM---- 243
Cy 243 RKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLR-GMGCAFVLYLDEIK 295
Db 244 -NSALGOYSSAGHCALTMLOKCGPRAFYKGFMPSTLRIGSNVNVFVTEQLKR 296

RESULT 14
US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF OBESITY
NUMBER OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-210-681-51

Query Match 14.6% Score 227; DB 3; Length 309;
Best Local Similarity 23.8% Pred. NO. 5e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

Cy 12 FLAGVAAVSTAVAPIERVKLLLOVHASK---QISAEKQKGIIDCVIRPKEGFL 68
Db 17 FLAGCTAACIADLITFPDITAKVRLIOGESGPPVATVSAOYKGMGTILTWRTGPR 76
Cy 69 SFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDYDRHKQFWRYPAGNLASGAGATSL 128
Db 77 SLVNGLVAGLOROMSFASVRIGLYDSVKQFYTKGEHNS-----IGSRLASTGTALAV 131
Cy 129 CFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSDGLGLYOGFNVSOGIITIRA 188
Db 132 AVAOPTDVAKVFQOARAGCGRRYOSTVNAVKTIARECGFGLMKGTSPNARNAIVNC 191
Cy 189 AVFGYVDTRAK-----GMLPRPKNNHIFVSMHIAOSVYAVACLLSPEDTVRRMMQSG 242
Db 192 AELVYTDLIKDALLANLMTDLPCH-FTSAFGAGCTTV---IASPDVVVTRTM---- 243
Cy 243 RKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLR-GMGCAFVLYLDEIK 295
Db 244 -NSALGOYSSAGHCALTMLOKCGPRAFYKGFMPSTLRIGSNVNVFVTEQLKR 296

RESULT 15
US-08-946-719A-51
Sequence 51, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-946-719A-51

Query Match 14.6% Score 227; DB 3; Length 309;
Best Local Similarity 23.8% Pred. No. 5e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

OY 12 FLAGAVAAAVSKTAVAPIERYKLLLOVQHASK---QISAERQYKGIIDCVVRIPEEGFL 68
D 17 FLAGGTACIADLITPLDTAKVRLIQGESQGPVRAVSAQYRGVWGTTLTWVTEGPR 76
OY 69 SFARGNLANVIRFPTQALNFAFDKYKQLFLGCVDRHKQFWRFFAGNLASGGAAGATSL 128
D 77 SLVNGLVAGLOROMSPASVRIGLYDSVKQFYTKGSEHAS-----IGSRLLAGSTTGALAV 131
OY 129 CFVYPLDPARTRLADYGRARQREFHGLGDCIIRKPSDGLRGLYOGFNVSYGIIITYRA 188
D 132 AVAOPDVVKRFOAQRAGGGRRYOSTVNAVYKTIAREEGFRGLMKGTSPVARNAIYVC 191
OY 189 AFGCVYDTAK-----GMLPDPKNVHIFVSWMIAOSYTAAGLSTYPPDVRRRMMQSG 242
D 192 AELVTYDLIKDALLKANLMTDDLPCF-FTSAFGAGFCTV---IASPVDVVKTRYM----- 243
OY 243 RKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLK-GMGAFVLYLYDEIKK 295
D 244 -NSALGOYSSAGICALTLMQKEGPRAFYKGFMPSEFLRLGSMNVVMFVTEQLKR 296

Search completed: June 18, 2003, 13:28:53
Job time : 17 secs

OY 181 OGIIYYRAAYFGVYDTAKGMLPDPKNVHI FVSWMIAOSVTAVAGLLSPDPTVRRMMQ 240
DB 181 OGIIYYRAAYFGVYDTAKGMLPDPKNVHI FVSWMIAOSVTAVAGLLSPDPTVRRMMQ 240
OY 241 SGRKADIMYTGTVDCMKRIAKDEGAKAFPGKAMSNVLRGKGAFVLVLYDEIKKYV 297
DB 241 SGRKADIMYTGTVDCMKRIAKDEGAKAFPGKAMSNVLRGKGAFVLVLYDEIKKYV 297

RESULT 2

US-09-811-094-31

Sequence 31, Application US/09811094

Patent No. US20010044144A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Cleveland, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Miller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Moos, Walter H.

APPLICANT: Pel, Yashong

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D4

CURRENT APPLICATION NUMBER: US/09/811.094

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 297

TYPE: PRT

ORGANISM: Homo sapien

US-09-811-094-31

Query Match

100.0%; Score 1553; DB 10; Length 297;

Best Local Similarity 100.0%; Pred. No. 2e-157;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVR 60
OY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
OY 121 GAAGATSLCFYVPLDFAFTRILAADVGRRAOREFHGLGCCIIFKSDGLRGLYGFNSV 180
DB 121 GAAGATSLCFYVPLDFAFTRILAADVGRRAOREFHGLGCCIIFKSDGLRGLYGFNSV 180
OY 181 OGIIYYRAAYFGVYDTAKGMLPDPKNVHI FVSWMIAOSVTAVAGLLSPDPTVRRMMQ 240
DB 181 OGIIYYRAAYFGVYDTAKGMLPDPKNVHI FVSWMIAOSVTAVAGLLSPDPTVRRMMQ 240
OY 241 SGRKADIMYTGTVDCMKRIAKDEGAKAFPGKAMSNVLRGKGAFVLVLYDEIKKYV 297
DB 241 SGRKADIMYTGTVDCMKRIAKDEGAKAFPGKAMSNVLRGKGAFVLVLYDEIKKYV 297

RESULT 3

US-09-810-644-31

Sequence 31, Application US/09810644

Patent No. US20020012992A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Cleveland, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Miller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Moos, Walter H.

APPLICANT: Pel, Yashong

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D3

CURRENT APPLICATION NUMBER: US/09/810.644

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 297

TYPE: PRT

ORGANISM: Homo sapien

US-09-810-644-31

Query Match

100.0%; Score 1553; DB 10; Length 297;

Best Local Similarity 100.0%; Pred. No. 2e-157;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVR 60
OY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
OY 121 GAAGATSLCFYVPLDFAFTRILAADVGRRAOREFHGLGCCIIFKSDGLRGLYGFNSV 180
DB 121 GAAGATSLCFYVPLDFAFTRILAADVGRRAOREFHGLGCCIIFKSDGLRGLYGFNSV 180
OY 181 OGIIYYRAAYFGVYDTAKGMLPDPKNVHI FVSWMIAOSVTAVAGLLSPDPTVRRMMQ 240
DB 181 OGIIYYRAAYFGVYDTAKGMLPDPKNVHI FVSWMIAOSVTAVAGLLSPDPTVRRMMQ 240
OY 241 SGRKADIMYTGTVDCMKRIAKDEGAKAFPGKAMSNVLRGKGAFVLVLYDEIKKYV 297
DB 241 SGRKADIMYTGTVDCMKRIAKDEGAKAFPGKAMSNVLRGKGAFVLVLYDEIKKYV 297

RESULT 4

US-09-185-904A-32

Sequence 32, Application US/09185904A

Patent No. US20020177185A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Cleveland, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Miller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAY

FILE REFERENCE: 660088.420

CURRENT APPLICATION NUMBER: US/09/185.904A

CURRENT FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 32

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapien

US-09-185-904A-32

Query Match

89.6%; Score 1391.5; DB 9; Length 298;

Best Local Similarity 88.6%; Pred. No. 3.4e-140;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVR 60
DB 1 MTDAAISFAKDFLAGAANAASKTAVAPIERVKLLQVOHASKOITADKOYKGIIDCVR 60


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OY 61 IPKEOGFLSFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDHRRKOFMRYPAGNLASG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 IPKEOEVLSEFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDKRTQFMRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADYGR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 GAAGATSLCFVYPLDFARTRLADYGR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
OY 180 VOGIIYRAAYFGVYDTAKGMLPDRKNVHIFVSMIAQSVTAVAGLSTYPPDTRRRMM 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 VOGIIYRAAYFGVYDTAKGMLPDRKNVHIFVSMIAQSVTAVAGLSTYPPDTRRRMM 240
OY 240 OSGRKGDIMYTGTDCKMRKIAKDEGAKAFPGAMSNVLRGAGAFVLVLYDEIKKY 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 OSGRKGDIMYTGTDCKMRKIAKDEGAKAFPGAMSNVLRGAGAFVLVLYDEIKKY 297

RESULT 5
US-09-811-094-32
: Sequence 32, Application US/09811094
: Patent No. US20010044144A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleveneger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pei, Yezhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.420D4
: CURRENT APPLICATION NUMBER: US/09/811,094
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 298
: TYPE: PRF
: ORGANISM: Homo sapien
US-09-811-094-32

Query Match      89.6% Score 1391.5; DB 10; Length 298;
Best Local Similarity 88.6%; Pred. No. 3,4e-140;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEOYKGIIDCVR 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MTDALSTFAKDFLAGVAAVSKTAVAPIERVKLLQVHASKQITADQYKGIIDCVR 60
OY 61 IPKEOGFLSFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDHRRKOFMRYPAGNLASG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 IPKEOEVLSEFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDKRTQFMRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADYGR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 GAAGATSLCFVYPLDFARTRLADYGR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
OY 180 VOGIIYRAAYFGVYDTAKGMLPDRKNVHIFVSMIAQSVTAVAGLSTYPPDTRRRMM 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 VOGIIYRAAYFGVYDTAKGMLPDRKNVHIFVSMIAQSVTAVAGLSTYPPDTRRRMM 240
OY 240 OSGRKGDIMYTGTDCKMRKIAKDEGAKAFPGAMSNVLRGAGAFVLVLYDEIKKY 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 OSGRKGDIMYTGTDCKMRKIAKDEGAKAFPGAMSNVLRGAGAFVLVLYDEIKKY 297

RESULT 6
US-09-810-644-32
: Sequence 32, Application US/09810644

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: Patent No. US20020012992A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleveneger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pei, Yezhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.420D3
: CURRENT APPLICATION NUMBER: US/09/810,644
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 298
: TYPE: PRF
: ORGANISM: Homo sapien
US-09-810-644-32

Query Match      89.6% Score 1391.5; DB 10; Length 298;
Best Local Similarity 88.6%; Pred. No. 3,4e-140;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEOYKGIIDCVR 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MTDALSTFAKDFLAGVAAVSKTAVAPIERVKLLQVHASKQITADQYKGIIDCVR 60
OY 61 IPKEOGFLSFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDHRRKOFMRYPAGNLASG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 IPKEOEVLSEFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDKRTQFMRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADYGR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 GAAGATSLCFVYPLDFARTRLADYGR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
OY 180 VOGIIYRAAYFGVYDTAKGMLPDRKNVHIFVSMIAQSVTAVAGLSTYPPDTRRRMM 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 VOGIIYRAAYFGVYDTAKGMLPDRKNVHIFVSMIAQSVTAVAGLSTYPPDTRRRMM 240
OY 240 OSGRKGDIMYTGTDCKMRKIAKDEGAKAFPGAMSNVLRGAGAFVLVLYDEIKKY 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 OSGRKGDIMYTGTDCKMRKIAKDEGAKAFPGAMSNVLRGAGAFVLVLYDEIKKY 297

RESULT 7
US-09-185-904A-33
: Sequence 33, Application US/09185904A
: Patent No. US20020177185A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleveneger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pei, Yezhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSA:
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 660088.420
: CURRENT APPLICATION NUMBER: US/09/185,904A
: CURRENT FILING DATE: 1998-11-03
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 33
: LENGTH: 298
: TYPE: PRF
: ORGANISM: Homo sapien

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RESULT 13
US-09-864-761-36440
: Sequence 36440, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aecomica-x-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 36440
: LENGTH: 87
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO L78810.1
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
: OTHER INFORMATION: EST_HUMAN HIT: P05141, EVALU6 6.00e-38
: OTHER INFORMATION: EST_HUMAN HIT: AW935235.1, EVALU6 5.00e-37
US-09-864-761-36440

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Query Match          25.9%; Score 402.5; DB 10; Length 87;
Best Local Similarity 87.4%; Pred No. 2e-35;
Matches 76; Conservative 8; Mismatches 2; Indels 1; Gaps 1;

Oy      113 FAGNLASGAGATSLCFVYPLDFARTRLADVGRR--AOREFHGLDCCIIFKSPDLRG 171
         ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1  FAGNLSACGAAGATSLCFVYPLDFARTRLADVGAAEREFRLGDCCIVKIKSPGICG 60

Oy      172 LYCGFNVSVOGIITYRAAYFGYYDTAK 198
         ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        61 LYCGFNVSVOGIITYRAAYFGIYDTAK 87

RESULT 14
US-09-777-921A-4
: Sequence 4, Application US/09777921A
: Patent No. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKUOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEIN
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FASTSEQ For Windows Version 4.0
SEQ ID NO 4
LENGTH: 475
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-777-921A-4

Query Match          22.6%; Score 350.5; DB 10; Length 475;
Best Local Similarity 32.3%; Pred. No. 7.1e-29;
Matches 95; Conservative 55; Mismatches 115; Indels 29; Gaps 9;

Oy      10 KDFLAGNAANAASKVAAPRIEVRKLLOVOHNSKOISAEKOYGKIIDCVNRIPKEGFLLS 69
         ||| : | | | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db     196 ROLLAGGAGAANSRSTAPLDRLKVMQGV-HOSKSNIIFGGFRQM-----KEGGRS 247

Oy      70 FWRCMLAVIRYPFOALNFPAFKDYKQLFLCQVBRHKQFMRYFAGCNLASGCAAGATSILC 129
         ||| | | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db    248 LMRIGCTVINIAPEATAKFMYEDYKKLLTPEGOKIGTFEERFISSM-----AGATAQT 302

Oy      130 FYVPIDFARTLADVARRAORREFHLDCDCIIKIFSDDGLKCLYOGFNVSVOGIITYRAA 189
         || : | : | | | | : | | : | | : | | : | | : | | : | | : | | : |
Db    303 FIYPMVEVKTRILA--VGKTGC--YSGIYDCAKKLIKLYEGFGFYGYVPNLLGIIIFYAGI 358

Oy      190 YFGYVDTK-----GMLPDPKNVHIIFVSMIMAOYSTAVAAGLSFPDVYRRRMQSGRK 244
         ||| : | | | : | | : | | : | | : | | : | | : | | : | | : |
Db    359 DLAVERYELSKSHWLNDFAKDSVNPGLVYLCCALSTSCQQLASTPALVTRTMOAOAMLE 418

Oy      245 GADMIVTYTDVCWRKLIADDEGAKAFPKKAMSNN---VLROMGCAFVLYLVLDIETIK 295
         || : | : | | | : | | : | | : | | : | | : | | : | | : | | : |
Db   419 GAPQL--NMVGLFRRIISKGLPGLRYGITPRFMKVLPAVGISY--VVYEENMKQ 468

RESULT 15
US-09-777-921A-2
: Sequence 2, Application US/09777921A
: Patent No. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKUOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEIN
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FASTSEQ For Windows Version 4.0
```

SEQ ID NO 2
LENGTH: 477
TYPE: PRT
ORGANISM: Homo sapiens
US-09-777-921A-2

Query Match 22.3% Score 346.5; DB 10; Length 477;
Best Local Similarity 32.7%; Pred. No. 1.9e-28;
Matches 96; Conservative 55; Mismatches 116; Indels 27; Gaps 10;

QY 10 KDLACAVAAVAVSTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVRIPEQGFLS 69
DB 196 RQLLAGGIAGAVSRTSTAPLDRLKIMQV-HGSK---SDKM-NIPGSPROMVKEGGIRS 249
QY 70 FWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDVRHKQFWRFYAGNLASGAAGATSLC 129
DB 250 LMRGNGTNVJKIAPETAVKFEMAYEQYKKLLTEEGCKICTFERFISGSM---AGATAOT 304
QY 130 FVYPLDFARPLADVGRRAQREPHGLGDCIIKIFKSDGLKGLYOGFNVSVQGIITYRAA 189
DB 305 FTYPMEVWKTRLA--VGKTGO--YSGIYDCAKKILKHGGLGAFYKGYVNPNLGITIYAGI 360
QY 190 YFGVYDTAK-----GMLPDPKNNVHIFVSMIAQSVTAVAGLLSTYPTDVRRRMMQSGRK 244
DB 361 DLAVYELLKSYWLDNPAKDSVNPQVWLLGGCALSTCCQLASTPLALVTRRMOQAQMLE 420
QY 245 GADIWYTGVDCKRRIAKDEGAKAFKGAWSN---VLKMGGAFLVLYDEIKK 295
DB 421 GSPQL--NMVGLFRRIISKEGICPLRYGIRTFNFMKVLPAVCISY--VVEENMKO 470

Search completed: June 18, 2003, 13:32:46
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:32:22 ; Search time 40 Seconds

(without alignments)
713.798 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDLAAGAVAAA.....LRGMCAGFVLVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1 A44778	ADP,ATP carrier pr
2	1466.5	94.4	298	2 I60173	adenine nucleotide
3	1463.5	94.2	298	2 S37210	ADP,ATP carrier pr
4	1458.5	93.9	298	1 XWBO	ADP,ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP,ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP,ATP carrier pr
7	1380.5	88.9	298	2 B43646	ADP,ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP,ATP carrier pr
9	1142.5	73.6	301	1 S31915	ADP,ATP carrier pr
10	1045.5	67.3	313	2 T25850	hypothetical prote
11	1043.5	67.2	313	2 T23207	hypothetical prote
12	1037.5	66.8	300	2 T25371	hypothetical prote
13	1005.5	64.7	300	2 T15206	hypothetical prote
14	973.5	62.7	339	2 A41677	ADP,ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP,ATP carrier pr
16	772	49.7	306	2 T20012	hypothetical prote
17	770.5	49.6	308	1 S30259	ADP,ATP carrier pr
18	756.5	48.7	387	2 S14876	ADP,ATP carrier pr
19	752.5	48.5	322	2 T40526	ADP,ATP translocas
20	752.5	48.5	386	2 T09709	ADP,ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP,ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP,ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP,ATP carrier pr
24	745.5	48.0	326	2 T25728	hypothetical prote
25	745.5	48.0	386	2 S17917	ADP,ATP carrier pr
26	744.5	47.9	386	2 S21974	ADP,ATP carrier pr
27	740	47.6	379	2 S21313	ADP,ATP carrier pr
28	740	47.6	386	2 S14874	ADP,ATP carrier pr
29	737	47.5	385	1 S29852	ADP,ATP carrier pr

30	736	47.4	307	2 A36582	ADP,ATP carrier pr
31	734	47.3	318	1 A31978	ADP,ATP carrier pr
32	733.5	47.2	313	1 XWNC	ADP,ATP carrier pr
33	729	46.9	305	2 S68154	ADP,ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP,ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP,ATP carrier pr
36	676	43.5	298	2 T24029	hypothetical prote
37	508	32.7	327	2 T51577	ADP,ATP translocas
38	368	23.7	415	2 T48171	hypothetical prote
39	367.5	23.7	325	2 T04273	hypothetical prote
40	363	23.4	381	2 T51158	hypothetical prote
41	350.5	22.6	475	2 T50686	peroxisomal Ca-dep
42	349.5	22.5	352	2 T01729	mitochondrial solu
43	345.5	22.2	358	2 T45934	hypothetical prote
44	334.5	21.5	348	2 D84798	probable mitochond
45	327	21.1	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1

A44778
ADP,ATP carrier protein T1 - human

N:Alternate names: mitochondrial ADP,ATP translocase 1

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence,Revision 17-Mar-2000 #text,Change 17-Mar-2000

C:Accession: A44778; S03893; A39891; A28116

R:Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Mae

J. Biol. Chem. 264, 13998-14004, 1989

A:Title: A human muscle adenine nucleotide translocator gene has four exons, 1s

A:Reference number: A44778; MUID:89340495; PMID:2547778

A:Accession: A44778

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <L1A>

A:Cross-references: GB:J02966; NID:g339919; PION:AAA51736.1; PID:g178659

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial AC

A:Reference number: S03893; MUID:89236396; PMID:2541251

A:Accession: S03893

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <CO2>

R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of

A:Reference number: A39891; MUID:86041145; PMID:2823266

A:Accession: A39891

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15, 'A', '17-146, 'RR', '149, '151-226, 'L', '228-298 <NEC>

A:Cross-references: GB:J02966; NID:g339919; PION:AAA61223.1; PID:g339920

R:Houldsworth, J.; Altardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA 1e

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: A28116

A:Molecule type: mRNA

A:Residues: 1-37 <HOU>

A:Cross-references: GB:J03593; NID:g339724; PION:AAA6751.1; PID:g339725

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT1; T1

A:Cross-references: GDB:119680; OMIM:103220

A:Map position: 4q35-4q35

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>

F:5-99/Domains: ADP,ATP carrier protein repeat homology <ACPI>

F:110-202/Domains: ADP,ATP carrier protein repeat homology <ACPI>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1: Length 298;
Best Local Similarity 98.3%; Pred. No. 1.6e-130;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
DB 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
OY 61 IREOGFLSFMKGNLANVIRYPTQALNFAPDKYKQFLGCVDRHKQFWRFFAGNLASG 120
DB 61 IREOGFLSFMKGNLANVIRYPTQALNFAPDKYKQFLGCVDRHKQFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCI1IKFSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCI1IKFSDGLRGLYOGFNV 180
OY 180 VOGI11YRAAYFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAAGLSTPPTVRRRMM 239
DB 181 VOGI11YRAAYFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAAGLSTPPTVRRRMM 240
OY 240 OSGRKADIMYTGTVDCMKRIKADGAKAFPGKAMSNTLRGCGAFVLYLDEIKKYV 297
DB 241 OSGRKADIMYTGTVDCMKRIKADGAKAFPGKAMSNTLRGCGAFVLYLDEIKKYV 298

RESULT 2

160173
adenine nucleotide translocator - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: 160173
R:Shiohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat
A:Reference number: 160173; MUID:94002161; PMID:8399300
A:Accession: 160173
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-298 <RES>
C:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
C:Genetics:
A:Gene: ant1
A:Introns: 37/3: 200/1: 247/1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2: Length 298;
Best Local Similarity 94.3%; Pred. No. 4.3e-125;

Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

OY 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
DB 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
OY 61 IREOGFLSFMKGNLANVIRYPTQALNFAPDKYKQFLGCVDRHKQFWRFFAGNLASG 120
DB 61 IREOGFLSFMKGNLANVIRYPTQALNFAPDKYKQFLGCVDRHKQFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCI1IKFSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCI1IKFSDGLRGLYOGFNV 180
OY 180 VOGI11YRAAYFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAAGLSTPPTVRRRMM 239
DB 181 VOGI11YRAAYFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAAGLSTPPTVRRRMM 240
OY 240 OSGRKADIMYTGTVDCMKRIKADGAKAFPGKAMSNTLRGCGAFVLYLDEIKKYV 297
DB 241 OSGRKADIMYTGTVDCMKRIKADGAKAFPGKAMSNTLRGCGAFVLYLDEIKKYV 298

DB 241 OSGRKADIMYTGTVDCMKRIKADGAKAFPGKAMSNTLRGCGAFVLYLDEIKKYV 298

RESULT 3
S37210
ADP,ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S37210
R:Laplace, C.; Costet, P.
Submitted to the EMBL Data Library, September 1993
A:Reference number: S37210
A:Accession: S37210
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <LAP>
C:Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628
C:Genetics:
A:Gene: ANCI
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2: Length 298;
Best Local Similarity 94.0%; Pred. No. 8e-125;

Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

OY 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
DB 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
OY 61 IREOGFLSFMKGNLANVIRYPTQALNFAPDKYKQFLGCVDRHKQFWRFFAGNLASG 120
DB 61 IREOGFLSFMKGNLANVIRYPTQALNFAPDKYKQFLGCVDRHKQFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCI1IKFSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCI1IKFSDGLRGLYOGFNV 180
OY 180 VOGI11YRAAYFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAAGLSTPPTVRRRMM 239
DB 181 VOGI11YRAAYFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAAGLSTPPTVRRRMM 240
OY 240 OSGRKADIMYTGTVDCMKRIKADGAKAFPGKAMSNTLRGCGAFVLYLDEIKKYV 297
DB 241 OSGRKADIMYTGTVDCMKRIKADGAKAFPGKAMSNTLRGCGAFVLYLDEIKKYV 298

RESULT 4

XMO
ADP,ATP carrier protein T1 - bovine

N:Alternate names: ADP/ATP translocase T1
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
C:Accession: A43646; A24822; A03181; A61343; S69269
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differ
A:Reference number: A43646; MUID:89229093; PMID:2540808
A:Accession: A43646
A:Molecule type: mRNA
A:Residues: 1-298 <POM>
C:Cross-references: GB:M24102; NID:g529414; PIDN:AA30768.1; PID:g529415
R:Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an
A:Reference number: A24822; MUID:86295775; PMID:3017341
A:Accession: A24822
A:Molecule type: mRNA
A:Residues: 208-298 <RAS>

A:Gene: GDB:ANT3: ANT3Y
 A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
 A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:2-298/Product: ADP,ATP carrier protein repeat homology <ACP1>
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP3>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 89.2%; Score 1385.5; DB 1: Length 298;
 Best Local Similarity 87.2%; Pred. No. 9,1e-118;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGVAAVASTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 1 MTEQAIISFAKDFLAGGIAAIAISTVAPIERVKLLQVHASKQIADQYKGIIDCVVR 60
 DB 1 MTEQAIISFAKDFLAGGIAAIAISTVAPIERVKLLQVHASKQIADQYKGIIDCVVR 60
 OY 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 DB 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 179
 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 180
 OY 180 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 239
 181 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 240
 DB 181 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 240
 OY 240 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297
 241 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 298
 DB 241 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 298

RESULT 7

B43646

ADP,ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R.Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A:Status: preliminary
 A:molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.9%; Score 1380.5; DB 2: Length 298;
 Best Local Similarity 86.9%; Pred. No. 2,6e-117;

Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGVAAVASTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 1 MTEQAIISFAKDFLAGGIAAIAISTVAPIERVKLLQVHASKQIADQYKGIIDCVVR 60
 DB 1 MTEQAIISFAKDFLAGGIAAIAISTVAPIERVKLLQVHASKQIADQYKGIIDCVVR 60
 OY 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 DB 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 179
 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 180

OY 180 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 239
 181 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 240
 DB 181 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 240
 OY 240 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297
 241 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 298
 DB 241 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 298

RESULT 8

S31814

ADP,ATP carrier protein T2 - mouse
 N:Alternate names: adenine nucleotide translocase
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
 C:Accession: S31814
 R.Costet, P.; Laplace, C.
 submitted to the EMBL Data Library, January 1993
 A:Reference number: S31814
 A:Accession: S31814
 A:Status: preliminary
 A:molecule type: mRNA
 A:Residues: 1-298 <COS>

A:Cross-references: EMBL:X70847
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.1%; Score 1368.5; DB 2: Length 298;
 Best Local Similarity 87.2%; Pred. No. 3,2e-116;

Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGVAAVASTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 1 MTEQAIISFAKDFLAGGIAAIAISTVAPIERVKLLQVHASKQIADQYKGIIDCVVR 60
 DB 1 MTEQAIISFAKDFLAGGIAAIAISTVAPIERVKLLQVHASKQIADQYKGIIDCVVR 60
 OY 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 DB 61 IPEOGFLSFMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 179
 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYOGFNNV 180
 OY 180 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 239
 181 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 240
 DB 181 VOGIIYYRAAYFGVYDTAKGMLPDPKNTIIFVSMIAQSVTAVAGVSPFDVRRRRMM 240
 OY 240 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 296
 241 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297
 DB 241 QSGRKADIMYGTVDCKMKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297

RESULT 9

S31935

ADP,ATP carrier protein - African malaria mosquito
 C:Species: Anopheles gambiae (African malaria mosquito)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S31935; S31936
 R:Beard, C.B.; Crews-Oyen, A.E.; Collins, P.H.
 submitted to the EMBL Data Library, February 1993
 A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
 A:Reference number: S31935
 A:Accession: S31935
 A:Status: preliminary
 A:molecule type: DNA
 A:Residues: 1-301 <BEA>

A:Cross-references: EMBL:221814; EMBL:221815
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:112-204/Domain:	ADP,ATP carrier protein repeat	homology <ACP2>
F:209-300/Domain:	ADP,ATP carrier protein repeat	homology <ACP3>

Query Match	73.6%	Score 1142.5;	DB 1;	Length 301;
Best Local Similarity	-76.2%;	Pred. No. 9.1e-96;		
Matches 221: Conservative	26;	Mismatches 42;	Indels 1;	Gaps 1;

[illegible]

RESULT 10

T25850

hypothetical protein T01B1.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

C:/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
C:/Accession: T25850
R/Gelsel, C.; Stellyes, L.

A:Description: The sequence of C. elegans cosmid T01b11 submitted to the EMBL Date library, December 1996

A:Reference number: Z20099

A:Accession: T25850

A:Status: preliminary; translated from GB/EMBL/DBJ

A: molecule type: DNA
 A: Residues: 1-113 <Get>
 A: Cross-references: EMBL:U080931; PTDN:AA838001.1; GSPDB:GND00022; CESP:T01B11.4
 A: Experimental source: strain Bristol N2; clone T01B11
 C: Genetics:
 A: Gene: CESP:T01B11.4
 A: Map position: 4
 A: Introns: 4/1: 191/2
 C: Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

[illegible]

RESULT 11

123207

hypothetical protein K01H12.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C/Accession: T23207
R/McMurray, A.
submitted to the EMBL Data Library, December 1995

A:Reference number: Z19/0/
A:Accession: T23207
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-313 <MIL>
A:Cross-references: EMBL:Z68218; PDB:CM92472.1; GSPDB:GN00022; CESP:K01H12.2
A:Experimental source: clone K01H12
C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A:Introns: 4/1, 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.2%; Score 1043.5; DB 2; Length 313;
Best Local Similarity 69.4%; Pred. No. 8.7e-87;
Matches 202; Conservative 37; Mismatches 49; Indels 3; Gaps 2;

Oy	8	FLKPLFLGAVAAASKTA	VAP1	ERVKLLLLLOVQ	HAAS1	SAKQVKGII	DCVARI	PRKEGF	67																									
Oy																																		
Db	25	FLIDLASGCTAAAS	KTA	VAP1	ERVKLLLOVQ	DSLT1	AADRKRG	IVDLYR	PKKEGY	84																								
Oy	68	LSFMKGNLANV1	RYFP	FOALNFA	ERDKYKOL	FLGCGVD	RHKOFMR	FAGNLAS	GGAAGATS	127																								
Oy																																		
Db	85	AALRGNSLANV1	RYFP	FOALNFA	ERDKYK	NI	FOKGLD	KXPMK	FFAGNLAS	GGAAGATS	144																							
Oy	128	LCFVYPLDFA	TRT	LAADVGR	BRARKE	EPHGLG	CCII	IK	FRSDGL	RCGLYOG	FNYSVGGII	YR	187																					
Oy																																		
Db	145	LCFVYPLDFA	TRT	LAADVGR	KANER	EPHGLG	ADLCV	LK	IAKSD	PP	IGLYR	CFPSVGGII	YR	204																				
Oy																																		
Oy	188	AAFGVYD	TAKGM	-	PDEKNV	HI	VS	WMI	AOS	YTA	VAG	LLSY	SPED	YVRR	MMQSG	RGA	246																	
Oy																																		
Db	205	AAFGMPT	TAKM	VFLAD	CKK	LN	PF	AA	IA	OV	Y	V	SG	CI	IS	Y	PMD	YVRR	MMQSG	RK	-	262												
Oy	247	DIMT	GV	AD	CKR	RI	AK	DE	GA	KA	PF	K	GA	S	N	L	R	CG	GA	F	V	L	Y	L	DE	I	K	K	Y	257				
Oy																																		
Db	263	DVLVKN	NT	DL	CA	V	K	I	I	KE	GA	S	AM	P	R	G	AL	S	N	Y	FR	CG	GA	F	V	L	Y	L	DE	I	K	K	Y	313

RESULT 12

T25371

hypothetical protein T27E9.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T25371
R;Lloyd, C.

Submitted to the EMBL Data Library, November 1996
A;Reference number: Z20024
A;Accession: T25371

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <Mile>
A:Cross-references: EMBL:282059; PIDD:CAM04874.1; GSPDB:GN00021; CESP:T27E9.1
A:Experimental source: clone T27E9
C:Genetics:
A:Gene: CESP:T27E9.1
A:Map position: 3
A:Introns: 20/1; 41/3; 115/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match	66.8%	Score 1037.5;	DB 2:	Length 300;
Best Local Similarity	69.1%	Pred. No. 2.9e-86;		
Matches 201: Conservative	38:	Mismatches 49:	Indels 3:	Gaps 2:

OY 8 FLKDFLAGAANAASVTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 67
 12 FLIDLASGCTAAAVSTAAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 71
 OY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAGATS 127
 72 AALMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAGATS 131
 OY 128 LCFVYPLDFARTRRLADVGRRAOREFHGLGDCIIFKSDGLRGLYOGFNVSVOGIIIVR 187
 132 LCFVYPLDFARTRRLADVGRRAOREFHGLGDCIIFKSDGLRGLYOGFNVSVOGIIIVR 191
 OY 188 AAFYGVYDTRAKGML-PDPKRVNHFVSMIAQSVTAAGLSTYPFQVRRRRMMQSGRKGA 246
 192 AAFYGVYDTRAKGML-PDPKRVNHFVSMIAQSVTAAGLSTYPFQVRRRRMMQSGRKGA 249
 OY 247 DIMYGTVDGMRKRIADDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYYV 297
 250 DILYKNTLDCAKKIIONEGKSNMFKGALSIVFRGTGALVLYLDEIQKFL 300

RESULT 13

T15206

hypothetical protein W02D3.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C:Accession: T15206

R:Le, T.; Weinstein, L.; Rifkin, L.

Submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans cosmid W02D3.

A:Reference number: 218308

A:Accession: T15206

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <LET>

A:Cross-references: EMBL:AF003141; NID:92088732; PID:92088738; PIDN:AA854179.1; GSPDB:GN

A:Experimental source: strain Bristol N2; clone W02D3

C:Genetics:

A:Gene: CESP:W02D3.6

A:Map position: 1

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

F:9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>

Query Match

Best Local Similarity 64.7%; Score 1005.5; DB 2; Length 300;

Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;

OY 8 FLKDFLAGAANAASVTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 67
 12 FLIDLASGCTAAAVSTAAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 71
 OY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAGATS 127
 72 AALMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAGATS 131
 OY 128 LCFVYPLDFARTRRLADVGRRAOREFHGLGDCIIFKSDGLRGLYOGFNVSVOGIIIVR 187
 132 LCFVYPLDFARTRRLADVGRRAOREFHGLGDCIIFKSDGLRGLYOGFNVSVOGIIIVR 191
 OY 188 AAFYGVYDTRAKGML-PDPKRVNHFVSMIAQSVTAAGLSTYPFQVRRRRMMQSGRKGA 246
 192 AAFYGVYDTRAKGML-PDPKRVNHFVSMIAQSVTAAGLSTYPFQVRRRRMMQSGRKGA 249
 OY 247 DIMYGTVDGMRKRIADDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYYV 297
 250 DILYKNTLDCAKKIIONEGKSNMFKGALSIVFRGTGALVLYLDEIQKFL 300

RESULT 14

A41677

ADP,ATP carrier protein - Chlorella kessleri

C:Species: Chlorella kessleri

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

C:Accession: A41677
 R:Highart, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A:Title: Glucose increases the expression of the ATP/ADP translocator and the 91
 A:Reference number: A41677; MUID:92084708; PMID:1748677
 A:Accession: A41677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-339 <HIL>
 A:Cross-references: GB:M76669; NID:9516596; PIDN:AA33027.1; PID:9516597
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; mitochondrion; transmembrane protein
 F:134-134/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:144-235/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:241-329/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 62.7%; Score 973.5; DB 2; Length 339;
 Best Local Similarity 65.3%; Pred. No. 2,1e-80;

Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;

OY 7 SFLKDFLAGAANAASVTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 64
 40 AFVKDLASGCTAAAVSTAAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 99
 OY 65 OGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAG 124
 100 OGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAG 158
 OY 125 ATSLCFVYPLDFARTRRLADVGRRAOREFHGLGDCIIFKSDGLRGLYOGFNVSVOGII 184
 159 ACSLLIYVPLDFARTRRLADVGRRAOREFHGLGDCIIFKSDGLRGLYOGFNVSVOGII 218
 DB 185 IYRAAYFGVYDTRAKGML-PDPKRVNHFVSMIAQSVTAAGLSTYPFQVRRRRMMQSGR 243
 219 VYRGAYFGVYDTRAKGML-PDPKRVNHFVSMIAQSVTAAGLSTYPFQVRRRRMMQSGR 276
 OY 244 KCADIMYGTVDGMRKRIADDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYYV 297
 277 -GGEROYNGTIDCMRVAOEGMKAFKFGAMSNVLRGMGAFVLYLDEIKKYYV 329

RESULT 15

S51132

ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)

N:Alternate names: ADP/ATP transporter

C:Species: Plasmodium falciparum

C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000

C:Accession: S51132

R:hatin, I.; Jauregui, G.

Eur. J. Biochem. 228, 86-91, 1995

A:Title: Molecular characterization of the ADP/ATP-translocator cDNA from the hum

A:Reference number: S51132; MUID:95188918; PMID:7883016

A:Accession: S51132

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-301 <HAT>

A:Cross-references: EMBL:X83551; NID:9623334; PIDN:CA58541.1; PID:9623335

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:6-102/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 58.2%; Score 904.5; DB 2; Length 301;
 Best Local Similarity 58.3%; Pred. No. 3,2e-74;
 Matches 172; Conservative 48; Mismatches 70; Indels 5; Gaps 4;

OY 7 SFLKDFLAGAANAASVTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 64
 40 AFVKDLASGCTAAAVSTAAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 99
 DB 65 OGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAG 124
 100 OGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPAGNLASGGAAG 158

Db 68 OGVLSLMRGVANVIRYEPPTQAFNFAFKDYFKNIF-PRYDONTDFSKEFCVNIISGATAG 126
QY 125 ATSLCFYVPLDFAFTRRLAADYGRAROREFHGLGDCIIRKRSDDLRLGLYOCFNVSOGII 184
Db 127 AISLLIYPLDFAFTRRLASDIDGKGRDROFTGLFDCLAKIYKOTGLSLISGSGVSVTGII 186
QY 185 IYRAAYFGVYDTAKGML-PDPKNVHI FVSNMIAOSYTA VAGLSTY PFDTVRRMMOSGR 243
Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKNVAOSVTILAGLISY PFDTVRRMMMSGR 246
QY 244 KG-ADIMYGTGDCMRKIADDEGAKAFFKGAMSNVLRGMGAFVLVLYDEIKKYV 297
Db 247 KGREIEIOYKNTIDCMIKILRNEGFGFGKAMANVIRGAGALVLFYDELQXLI 301

Search completed: June 18, 2003, 13:36:47
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: June 18, 2003, 13:28:56 ; Search time 22 Seconds

(without alignments)
559,930 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAAA.....LRMGCAFVLVLDKIKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	1 ADT1_HUMAN	P12235 homo sapien
2	1466.5	94.4	298	1 ADT1_RAT	O05962 rattus norv
3	1463.5	94.2	298	1 ADP1_MOUSE	P48962 mus musculu
4	1453.5	93.6	297	1 ADT1_BOVIN	P02722 bos taurus
5	1408.5	90.7	298	1 ADT2_MOUSE	P51881 mus musculu
6	1407.5	90.6	298	1 ADT2_RAT	O09073 rattus norv
7	1398.5	90.1	298	1 ADT2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	1 ADT3_HUMAN	P12236 homo sapien
9	1380.5	88.9	298	1 ADT3_BOVIN	P32007 bos taurus
10	1211	78.0	297	1 ADT1_DROME	O26365 drosophila
11	1162.5	74.9	301	1 ADT1_ANOGA	O27238 anopheles g
12	973.5	62.7	339	1 ADT1_CHLKE	P31692 chlorella k
13	770.5	49.6	308	1 ADT1_CHLRE	P27080 chlamydomon
14	756.5	48.7	387	1 ADT1_MAIZE	P04709 zea mays (m
15	753.5	48.5	322	1 ADT1_SCHPO	O09188 schizosach
16	752.5	48.5	386	1 ADT1_GOSHI	O22342 gossypium h
17	751.5	48.4	382	1 ADT1_ORYSA	P31691 oryza sativ
18	751.5	48.4	387	1 ADT2_MAIZE	P12857 zea mays (m
19	746	48.0	381	1 ADT1_ARATH	P13167 arabidopsis
20	744.5	47.9	386	1 ADT1_SOLTU	P25083 solanum tub
21	742.5	47.8	331	1 ADT1_MHEAT	O41629 triticum ae
22	740	47.6	386	1 ADT2_SOLTU	P27081 solanum tub
23	736	47.4	307	1 ADT3_YEAST	P18238 saccharomyc
24	734	47.3	318	1 ADT2_YEAST	P18239 saccharomyc
25	733.5	47.2	313	1 ADT1_NEUCR	P40941 neurospora
26	731	47.1	385	1 ADT2_ARATH	P49382 kluyveromyc
27	729	46.9	305	1 ADT1_KLUUA	O41630 triticum ae
28	728.5	46.9	331	1 ADT2_MHEAT	P04710 saccharomyc
29	718.5	46.3	309	1 ADT1_YEAST	O75746 homo sapien
30	302.5	19.5	678	1 CMC1_HUMAN	GDC_BOVIN
31	300.5	19.3	330	1 GDC_BOVIN	GDC_BOVIN
32	296.5	19.1	702	1 CMC1_CAEBL	O21153 caenorhabdi
33	296	19.1	588	1 CMC2_CAEBL	O20799 caenorhabdi

34	295	19.0	322	1 GDC_RAT	P16261 rattus norv
35	292.5	18.8	307	1 ODC2_YEAST	O99297 saccharomyc
36	292	18.8	332	1 GDC_HUMAN	P16260 homo sapien
37	291	18.7	675	1 CMC2_HUMAN	O9ujs0 homo sapien
38	286	18.4	587	1 CMC3_CAEBL	O19529 caenorhabdi
39	280	18.0	315	1 MPT_HUMAN	O9hxd1 homo sapien
40	279.5	18.0	676	1 CMC2_MOUSE	O9qxx4 mus musculu
41	270.5	17.4	315	1 SA18_HUMAN	O9h1k4 homo sapien
42	267.5	17.2	325	1 UCP5_MOUSE	O9z2b2 mus musculu
43	266.5	17.2	310	1 ODC1_YEAST	O03028 saccharomyc
44	265.5	17.1	325	1 UCP5_HUMAN	O95258 homo sapien
45	263.5	17.0	695	1 CMC1_DROME	O9va73 drosophila

ALIGNMENTS

RESULT 1	ID	ADT1_HUMAN	STANDARD:	PRT:	298 AA.
AC	P12235:				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).				
GN	SLC25A4 OR ANT1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=89236396; PubMed=2541251;				
RA	Cozens A.L., Runswick M.J., Walker J.E.;				
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";				
RT	J. Mol. Biol. 206:261-280(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=89340499; PubMed=2547778;				
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;				
RT	"A human muscle adenine nucleotide translocator gene has four exons, and is located on chromosome 4, and is differentially expressed.";				
RT	J. Biol. Chem. 264:13998-14004(1989).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=86041149; PubMed=2823266;				
RA	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;				
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE-EYE:				
RC	Strausberg R.;				
RA	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE OF 1-37 FROM N.A.				
RP	TISSUE=LIVER:				
RC	MEDLINE=88124845; PubMed=2829183;				
RA	Houldsworth J., Altardi G.;				
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).				
RN	[6]				
RP	VARIANTS PEO PRO-114 AND MET-289.				
RP	MEDLINE=20385067; PubMed=10926541;				
RA	Kaukonen J., Jusselien J.K., Tiranti V., Kyttala A., Zeviani M., Cont G.P., Kertanen J., Pellonen L., Suomalainen A.;				
RT	"Role of adenine nucleotide translocator 1 in mtDNA maintenance.";				


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RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RL Biochemistry 28:866-873(1989).
RN 12)
RX SEQUENCE.
RX Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN 13)
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE-86295775; Pubmed-3017341.
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3' noncoding sequence."
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A03181; XMOO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; Mito_carr_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER_3.
KN Mitochondrion: Inner membrane: Repeat: Transmembrane: Transport;
KN Multigene family: Methylation.
FT INIT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match 93.6%; Score 1453.5; DB 1; Length 297;
Best Local Similarity 94.6%; Pred. No. 1; 1e-125;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 3 DHAMSLKDFLAGAANAASKTAVADIERVKLLQVOHSAKQISAQKYGKIIDCVVRIP 62
DB 2 DQALSLKDFLAGAANAASKTAVADIERVKLLQVOHSAKQISAQKYGKIIDCVVRIP 61
OY 63 KEGGLSPFMRGNLANIYRFPFOALNFAFKDKYKOLFICGVDRHKKFMRFRFAGNLASGGA 122
DB 62 KEGGLSPFMRGNLANIYRFPFOALNFAFKDKYKOLFICGVDRHKKFMRFRFAGNLASGGA 121
OY 123 AGATSLCFVYPPLDFARTRLAADGR-RAOREFHGLGDCDIKIKFSGLGLVOCGFVNSVO 181
|||||

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DB 122 AGATSLCFVYPPLDFARTRLAADYKCAAOEFETGLCNCITKIKRSDGLRCLYOCGFVNSVO 181
OY 182 GIITTYRAAYEGVYDTAKGMLPDPKNVHI FVSMWIAOSVTAAGLLSYPFDTVRRMQOS 241
DB 182 GIITTYRAAYEGVYDTAKGMLPDPKNVHI TVSMWIAQVTAAGLVSPFDTVRRMQOS 241
OY 242 GRGADIMTYGTDCMKRIKDEGAKAFKFGANSNVLKRGCAFVLVYDEIKKYV 297
DB 242 GRGADIMTYGTDCMKRIKDEGPKAFKFGANSNVLKRGCAFVLVYDEIKKFV 297

RESULT 5
ADP2_MOUSE STANDARD: PRT: 298 AA.
ID ADP2_MOUSE
AC P51881; 061311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE-97059403; Pubmed-8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Costet P., Laplace C.;
RL Submitted (Feb-1993) to the EMBL/Genbank/DBJ databases.
RN [4]
RP REVISIONS.
RA Laplace C.;
RL Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-20432087; Pubmed-10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes."
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27316; AAC52838.1; -
DR EMBL: U10404; AAA19009.1; -
DR EMBL: X70847; CAA50196.1; -

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RX MEDLINE-90375457; PubMed-2168878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurel J.;
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular
 cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87166056; PubMed-3031073;
 RA Bactini R., Ferrati S., Kaczmarek L., Calabretta B., Chen S.T.,
 RA Baserga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
 growth-regulated.";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Baybayan P., Strano A., Nagaraia R.,
 RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozerky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE-88124845; PubMed-2829183;
 RA Houdsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC -----
 CC
 DR EMBL: M57424; AAA51737.1; -
 DR EMBL: J02683; AAA35579.1; -
 DR EMBL: L78810; AAB39266.1; -
 DR EMBL: AC004000; AAB96347.1; -
 DR EMBL: J03591; AAA36749.1; -
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR Genew: HGNC:10991; SLC25A5.
 DR MIM: 300150; -
 DR Interpro: IPR002067; Mit_carrier.
 DR Interpro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCHARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT

FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973CAED92C49D3 CRC64;
 Query Match 90.1%; Score 1398.5; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 1.2e-120;
 Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;
 OY 1 MCDHMSFLKDFLAGAANAASVAVAPLERYKLLQVOHASKQISAEROKYKGIIDCVRR 60
 1
 DB 1 MDDAIVSFAKDFLAGAANAASVAVAPLERYKLLQVOHASKQI7ADKQYKGIIDCVRR 60
 OY 61 IREKGFSLFMRGNLANVIRYPTQALNFAFDKTKQLFLGCVDRHKQFRRPAGNLASG 120
 1
 DB 61 IREKGFSLFMRGNLANVIRYPTQALNFAFDKTKQLFLGCVDRHKQFRRPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDPARTRLADYGRR-AOREPFGICGCI1KIFKSDGLRGLYOGFNV 179
 1
 DB 121 GAAGATSLCFVYPLDPARTRLADYGRR-AOREPFGICGCI1KIFKSDGLRGLYOGFNV 179
 OY 180 VGGI1YRAAFPGVYDTAKGMLPDPKNNH1FVSWN1AOSVTAAGLSTPFDVRRMM 239
 1
 DB 181 VGGI1YRAAFPGVYDTAKGMLPDPKNNH1FVSWN1AOTVTAAGLSTPFDVRRMM 240
 OY 240 OSGRGADIMTGTVDCKRKIAKDGAKAFKFGANSVLRGCGAFVLVDEIKY 296
 1
 DB 241 OSGRGADIMTGTVDCKRKIAKDGAKAFKFGANSVLRGCGAFVLVDEIKY 297
 RESULT 8
 ADT3_HUMAN
 ID ADT3_HUMAN STANDARD: PRT; 298 AA.
 AC P12236; Q96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform 12 (ADP/ATP translocase 3)
 GN SLC25A6 OR ANT3.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89236396; PubMed-2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain, Cervix, Eye, and Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE-88124845; PubMed-2829183;
 RA Houdsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.

```

CC      -|- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC      -|- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-----
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CC      or send an email to license@isb.sib.ch.
-----
DR      EMBL: J03592; AAA6750.1; -.
DR      EMBL: AY007135; AACG198.1; -.
DR      EMBL: BC007285; AAH07285.1; -.
DR      EMBL: BC007850; AAH07850.1; -.
DR      EMBL: BC008737; AAH08737.1; -.
DR      EMBL: BC008935; AAH08935.1; -.
DR      EMBL: BC014775; AAH14775.1; -.
DR      PIR: S03894; S03894.
DR      PIR: B28116; B28116.
DR      Genew: HGNC:10992; SLC25A6.
DR      MIM: 300151; -.
DR      MIM: 403000; -.
DR      InterPro: IPR002067; Mit_carrier.
DR      InterPro: IPR001993; Mitoch_carrier.
DR      Pfam: PF00153; mito_carr; 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PROSITE: PS00215; MITOCH_CARRIER; 3.
KW      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
KW      Multigene family.
FT      TRANSMEM 12 29 1 (POTENTIAL).
FT      TRANSMEM 73 91 2 (POTENTIAL).
FT      TRANSMEM 117 134 3 (POTENTIAL).
FT      TRANSMEM 176 195 4 (POTENTIAL).
FT      TRANSMEM 214 231 5 (POTENTIAL).
FT      TRANSMEM 273 291 6 (POTENTIAL).
FT      REPEAT 1 100 1.
FT      REPEAT 101 208 2.
FT      REPEAT 209 298 3.
FT      CONFLICT 105 108 KHTO -> RHA (IN REF. 4).
FT      CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
SQ      SEQUENCE 298 AA: 32866 MW: 18534E9F0E49672P CXC64;

Query Match          89.2%; Score 1385.5; DB 1; Length 298;
Best Local Similarity 87.2%; Pred. No. 1.8e-119;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY      1 MGHANSEFLDFLAGVAANAASKRAVAPIEVKLLLOVOHAKSKQISAEKQTKGIIDCYVR 60
        I : I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
DB      1 MTEDAIIFAFDFLAGIAAAISKTAVANPIERVKLLLOVHNSKOIAADKOVKGIVDCIVR 60
QY      61 IPKRGESLFSPFGNLANVIYRYEPFOALFAFKDKYKOLFGVDNRHKOFMYRFAGNLASG 120
        I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
DB      61 IPKRGCVLSFPGRGLANVIIRFFPOALNFAPKDKYKQIFLGVDNKHPFRYFACNLASG 120
QY      121 GAACATSLCFPYPLDFARTRLAADVGRR-AQREFHGJGDCTIKIFKSDGLKGLYGGFNV 179
        I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
DB      121 GAACATSLCFEYPYPLDFARTRLAADVGKSGTEREPRLGDLCLVTIKSDGIRGLYOGFSVS 180
QY      121 VOGIIITRAAYFCGYTPRAKGLPPPKKNVHIFVSNMIAOSYAVAVAGLSTPRDYTRRRMM 239
        I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
DB      181 VOGIIITRAAFGYVDPAKGLPPPKKNHIVYSNMIAQTVAVAVGVSYPRDYTRRRMM 240
QY      240 OSGRKGADIMYTGVDDCMRKIAKDEGAKAFFKGSANVLKRMGAFFYLVLDELTKKYV 297
        I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
DB      241 OSGRKGADIMYTGVDDCMRKIRFREDGKAFKFGKAMSNNLRMGCAFYLVLYDELKKVI 298

RESULT 9
ADT3_BOVIN
ID     ADT3_BOVIN           STANDARD:       PRT:   298 AA.
AC     P32007;
DT     01-JUL-1993 (Rel. 26, Created)

```

DT	01-Jul-1993 (Rel. 26, Last sequence update)
DT	16-Oct-2001 (Rel. 40, Last annotation update)
DE	ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT3).
GN	SLOC25A6 OR ANT3.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A..
RX	MEDLINE=69229093; PubMed=2540808;
RA	Powell S.J., Medd S.M., Runswick M.J., Walker J.E.:
RT	"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues."
RL	Biochemistry 28:866-873(1989).
CC	-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC	-!- SUBUNIT: HOMODIMER.
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC	-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC	-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC	-----
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CC	-----
DR	EMBL; M24103; AAA30769.1; ..
DR	PIR; B43646; B43646.
DR	InterPro; IPR002067; Mt_carrier.
DR	InterPro; IPR001993; Mitoch_carrier.
DR	Pfam; PF00153; mito_carr; 3.
DR	PRINTS; PR00926; MITOCARRIER.
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multigene family.
FT	TRANSMEM 12 29 1 (POTENTIAL).
FT	TRANSMEM 73 91 2 (POTENTIAL).
FT	TRANSMEM 117 134 3 (POTENTIAL).
FT	TRANSMEM 176 195 4 (POTENTIAL).
FT	TRANSMEM 214 231 5 (POTENTIAL).
FT	TRANSMEM 273 291 6 (POTENTIAL).
FT	REPEAT 12 111 1.
FT	REPEAT 112 208 2.
FT	REPEAT 209 298 3.
SO	SEQUENCE 298 AA; 32877 MW; 1C34EFDFFEDE4061 CRC64;
Query Match	88.9%; Score 1380.5; DB 1; Length 298;
Best Local Similarity	86.9%; Pred. No. 5,1e-119;
Matches 259;	Conservative 21; Mismatches 17; Indels 1; Gaps 1.
OY	1 MGDIANSLKPLKGLGCAVAAASKTPNAVAPIEVKLLLOVQHASKOTSAAKOYKGITDCVR 60
DB	1 MTEOAIISFAKFOGLAGIAAMAISKVANAPIEVKKLLLOVAHAKOIAADOKYKGIVDCIVR 60
OY	1 IPKRGCLSPFGRNLANYIRFPPOALNFAPFKDKYUKOLFSGVDNRHKOFMYRFAGNLASG 120
DB	61 IPKRGCVLSFGRNLANYIRFPPOALNFAPFKDKYUOLFLGSGVDNRKFPMYRFAGNLASG 120
OY	121 GAAGATSLCEFYVPILDPAFTRILAADVGR-AOREFHGLSDCTIIKIFKSDGLNGLYOGFNVS 179
DB	121 GAAGATSLCEFYVPILDPAFTRILAADVGRSGSEREFGLSDCTLVKITSDSIGIRGLYOGFNVS 180
OY	180 VGGIITRYAAAFGVYDDPAKGMILPRPKNVHIVSNMIAQSNAVAVGLSYPDYVRRMM 239
DB	181 VGGIITRYAAAFGVYDDPAKGMILPRPKNVHIVSNMIAQTVAVAGVWSYPDYVRRMM 240


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Db      159  AGSLIVYPLDFAKRTLADVSGKSRFTGLVDCLSKYKGGPALKOGGVSOGII 218
      185  IYRAAFGVYDTAKGML-PDPKNVHIFVSMIAOSYAVAGLLSPFDVRRMMQSR 243
      219  VYRGAVFGLYDTAKGVLFDKERTANFFAKMAVAQAVTAGAGVLSYDFDVRRLMOS-- 276
Oy      244  KGADIMYTGTVDCMKRIADDEGAKAFKCAMSNVLRGKGAFVLYLDEIKTY 297
      277  -GGEROYNGTIDCMRKVVAOOGKAFKCAMSNVLRGAGAFVLYLDEIKTY 329

RESULT 13
ADT_CHLRE  STANDARD:  PRT:  308 AA.
ID  ADT_CHLRE
AC  P27080;
DT  01-AUG-1992 (Rel. 23, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DT  01-OCT-1994 (Rel. 30, Last annotation update)
DE  ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide
DE  translocator) (ANT).
GN  ABT.
OS  Chlamydomonas reinhardtii.
OC  Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC  Chlamydomonadaceae; Chlamydomonas.
OX  NCBI_TaxId=3055;
RN  11)
RP  SEQUENCE FROM N.A.
RC  STRAIN=FUD4-R2;
RX  MEDLINE=93204887; PubMed=8455552;
RA  Sharpe J.A., Day A.;
RT  Structure, evolution and expression of the mitochondrial ADP/ATP
RT  translocator gene from Chlamydomonas reinhardtii."
RL  Mol. Gen. Genet. 237:134-144(1993).
CC  -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC  MITOCHONDRIAL INNER MEMBRANE.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC  inner membrane.
CC  -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC  -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC
DR  EMBL: X65194; CAA46311.1; -
DR  PIR: S30259; S30259.
DR  InterPro: IPR002067; Mtl_carrier.
DR  Pfam: PF00153; Mito_carrier.3
DR  PRINTS: PR00926; MITOCARRIER.
DR  PROSITE: PS00215; MITOCH_CARRIER_2.
KW  Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT  TRANSMEM 12 29 1 (POTENTIAL).
FT  TRANSMEM 74 92 2 (POTENTIAL).
FT  TRANSMEM 116 133 3 (POTENTIAL).
FT  TRANSMEM 178 197 4 (POTENTIAL).
FT  TRANSMEM 217 234 5 (POTENTIAL).
FT  TRANSMEM 273 291 6 (POTENTIAL).
SQ  SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 49.6%; Score 770.5; DB 1; Length 308;
Best local Similarity 52.6%; Pred. No. 3,4e-63;
Matches 159; Conservative 49; Mismatches 77; Indels 17; Gaps 6;
Oy      7  SFLKDLFAGVAANAASKTAVAPIERVKLLQVO-HASKOISAEKQYGIIDCVRIKPO 65
      7  NFNVDFLAGGLSAAVASKTAAPIERVKLLIQNDENIKGRLASPYKGIQGEFVRVREE 66

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Oy      66  CFLSWRGLNAVIRFPPOALNFAFKKYKOLPLAGDNRHKNFRYFAGNLASGACGA 125
      67  GFGSLMRGNTAVJIRFPPOALNFAFKDKFKMF--GFKDKDEYKWFAGNMAAGACGA 124
Db      126  TSLCFYVPLDFAKRTLAADVGR----AOREFHGLDCCI1K1FKSDGJLGLVQGNVSVQ 181
      125  VSLSFYSLDVARTRLANAKSAKKGCGGROFNGLDVYRKRTJASDGIAGLYRGFNISCV 184
Oy      182  GIIYRAAFGVYDTAKG-MLPDPKNVHIFVSMIAOSYAVAGLLSPFDVRRMMQ 240
      185  GIVYRGVGLFYGMYDSLKPVLVGLPLANNFLAFLGKGTIGAGLASVYIDTIRRMHMT 244
Oy      241  SGRKGADIMYTGTVDCMKRIADDEGAKAFKCAMSNVLRGKGAFVLYLDEI-----K 294
      245  S--GSAVKYNSSFHCFOEIVNKGKSLFKGAGANILRAVAGVLAGYDLOVILLCK 301
Oy      295  KY 296
      302  KY 303
Db

RESULT 14
ADT1_MAIZE  STANDARD:  PRT:  387 AA.
ID  ADT1_MAIZE
AC  P04709;
DT  13-AUG-1987 (Rel. 05, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  ADP/ATP carrier protein 1, mitochondrial precursor (ADP/ATP
DE  translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN  ANT1 OR ANT-G1.
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC  Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxId=4577;
RN  11)
RP  SEQUENCE FROM N.A.
RC  STRAIN=MUTIND-FR7205034;
RX  MEDLINE=91322533; PubMed=1863785;
RA  Winning B.M., Day C.D., Sarah C.J., Leaver C.J.;
RT  Nucleotide sequence of two cDNAs encoding the adenine nucleotide
RT  translocator from Zea mays L."
RL  Plant Mol. Biol. 17:305-307(1991).
RN  12)
RP  SEQUENCE OF 59-387 FROM N.A.
RC  STRAIN=CV. B37N;
RX  MEDLINE=89338399; PubMed=2547608;
RA  Leaver C.J., Balgate B., Baker A.;
RT  "Two genes encode the adenine nucleotide translocator of maize
RT  mitochondria. Isolation, characterisation and expression of the
RT  structural genes."
RL  Eur. J. Biochem. 183:303-310(1989).
RN  13)
RP  SEQUENCE OF 70-387 FROM N.A.
RC  MEDLINE=85297781; PubMed=2994015;
RA  Baker A., Leaver C.J.;
RT  "Isolation and sequence analysis of a cDNA encoding the ATP/ADP
RT  translocator of Zea mays L."
RL  Nucleic Acids Res. 13:5857-5867(1985).
CC  -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC  MITOCHONDRIAL INNER MEMBRANE.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondria)
CC  inner membrane.
CC  -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC  -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC or send an email to license@isb-sib.ch).

[illegible]

RESULT 15	ADT_SCHPO	STANDARD:	PRT:	322 AA.
ADT_SCHPO				
ID	ADT_SCHPO			
AC	009186:			
DT	01-NOV-1997 (Rel. 35, Created)			
DJ	01-NOV-1997 (Rel. 35, Last sequence update)			
DJ	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide			
DE	translocator) (ANT).			
GN	ANCI OR SPBC530.10C.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetes.			

Best Local Similarity 52.9%; Pred. No. 16e-61;
Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;

```

OY 7 SFLKDFLAGAVAAVSKTAVAPIERVKLLLOVQHASKOISAEK--QYKGIIDCVRIIPK 63
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 26 TFFFDPMGCVSAASVSKTAAPIERVKLLIQNQ--DEMIKAGRLSHRYKIGICECFKRTAA 83
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 64 EOGFLSFMRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHKQFWRYPAGNLAGGAA 123
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 84 ECGVISTLMRGNTANLRYFPTQALNFAFKDKFKMF-GYKKERDGYAKWFGNLAGGAA 142
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 124 GATSLCFVYPLDFARTRLAAD--VGRAROREPHGIGDCIITKIFKSDGLRGLYOGPNVSV 180
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 143 GAASLFLVYSLDYARTRLANDAKSAKGGEROFNGLDVYRKTYRSDGLRGLYRGFGPSV 202
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 181 OGIIYRAAYFCVYDTAKG-MLPDPKNVHI FVSWMI AOSVTAACLLSYFPDVTVRMM 239
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 203 VGIIVYRGLYFGMYDTLKPVYLVGPLEGNFLASFLGMAVTTGSGCVASYPLDTIRRM 262
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY 240 OSGRKGADIMYTGTVDCMRKIIAKDEGAKAFKAGANSNVLKMGCAFVLVYDEIK 294
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 263 TSGEA---VKYSSSECGROI LAKEGARSFKAGAGANILRGVAGAGVLSIYDOVO 314
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

Search completed: June 18, 2003, 13:34:32
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2003, 13:31:32 ; Search time 80 Seconds
(without alignments)
764.950 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHANSFLKDFLAGVAAA.....LRGMCAGFVLVYDEIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMEL_21:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mhbc:*
9: SP_organelle:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_rvirus:*
16: SP_bacteriopl:*
17: SP_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464.5	94.3	298	6	O46373
2	1463.5	94.2	298	11	O62164
3	1411.5	90.9	298	6	O8SQH5
4	1377.5	88.7	298	13	O91YC4
5	1377.5	88.7	298	13	O9PRH1
6	1374.5	88.5	298	13	O9PRH2
7	1366.5	88.0	298	13	O919M9
8	1245.5	80.2	299	5	O95VX4
9	1241.5	79.9	300	5	O9NHWS
10	1241.5	79.9	299	5	O9SS30
11	1234.5	79.5	317	13	O91336
12	1183	76.2	288	5	O44093
13	1183	76.2	288	5	O44094
14	1147	73.9	307	5	O62526
15	1139.5	73.4	304	5	O25129
16	1101.5	70.9	315	4	O9HOC2

17	1045.5	67.3	313	5	P91410
18	1043.5	67.2	313	5	O21103
19	1037.5	66.8	300	5	O45865
20	1005.5	64.7	300	5	O01813
21	993.5	64.0	300	5	O17407
22	989.5	63.7	309	5	O97470
23	959	61.8	307	8	O9XM22
24	950	61.2	318	5	O9B336
25	905.5	58.3	301	5	O25692
26	904.5	58.2	301	5	O26006
27	841.5	54.2	170	6	O9X569
28	772	49.7	306	5	O18683
29	757.5	48.8	305	3	O9PM1
30	750.5	48.3	307	5	O76286
31	748.5	48.2	303	3	O74260
32	746.5	48.1	379	10	O49447
33	745.5	48.0	326	5	P91270
34	743.5	47.9	307	5	O26697
35	740.5	47.7	386	10	P93767
36	738.5	47.6	388	10	O49875
37	731.5	47.1	317	5	O9N647
38	728.5	46.9	306	3	P78754
39	727.5	46.8	331	10	O41628
40	708	45.6	305	3	O9P876
41	705	45.4	305	3	O9P875
42	698	44.9	308	3	O8TF87
43	681	43.9	330	10	O9FM86
44	676	43.5	298	5	O21809
45	659	42.4	262	10	O9AVT6

ALIGNMENTS

RESULT 1					
O46373	ID	O46373	PRELIMINARY:	PRT:	298 AA.
AC	O46373:				
DT	01-JUN-1998 (TREMBL)	06, Created)			
DT	01-JUN-1998 (TREMBL)	06, Last sequence update)			
DT	01-MAR-2002 (TREMBL)	20, Last annotation update)			
DE	ADP/ATP translocase.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_Taxid:9986;				
RN	[1]				
RP	SEQUENCE FROM N. A.				
RC	TISSUE=SKLETAL MUSCLE;				
RA	Yamauchi N., Kasai M.				
RT	"Identification of a 30kDa calsequestrin-binding protein, which				
RT	regulates calcium release from sarcoplasmic reticulum of rabbit				
RT	skeletal muscle."				
RL	J. Biochem. 335:541-547(1998).				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL				
CC	INNER MEMBRANE (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
CC	EMBL: AB009386; BAA23777.1;				
DR	InterPro: IPR001993; Mitoch carrier.				
DR	InterPro: IPR002067; Mit carrier.				
DR	Pfam: PF00153; mito_carr; 3.				
DR	PRINTS: PR00926; MITOCARRIER.				
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.				
KW	Inner membrane; Mitochondrion; Transmembrane; Transport.				
SO	SEQUENCE 298 AA; 32901 MW; CAEAJ2C88164AD78 CRC64;				
Query Match	94.38;	Score 1464.5;	DB 6;	Length 298;	
Best Local Similarity	94.68;	Pred. No. 6.2e-126;			
Matches 282;	Conservative	7;	Mismatches 8;	Indels 1;	Gaps 1;
Oy	1	MGDANSFLKDFLAGVAAVSKRAVPPIRVKLLLOVONASKOISAEKQYKGIIDCVR	60		
Db	1	MSDQALSLKDFLAGVAAVSKRAVPPIRVKLLLOVONASKOISAEKQYKGIIDCVR	60		

Oy	6	1PEQGEFLSPMREGLNLANVRYEPTQALNPAFDKXKOLFJGCVBRHKOFRYPAGNLASG	120
Dh	61	1PEQGEFLSPMREGLNLANVRYEPTQALNPAFDKXKOLFJGCVBRHKOFRYPAGNLASG	120
Oy	121	GAAGATSLCFVYPLPFPARTPLAADVGR-RAOREFHGLDCDCKIKTFSKSDGLRGLOCGNNYS	179
Dh	121	GAAGATSLCFVYPLPFPARTPLAADVGR-RAOREFHGLDCDCKIKTFSKSDGLRGLOCGNNYS	179
Oy	122	GAGCATSLCFVYPLPFPARTPLAADVGR-RAOREFHGLDCDCKIKTFSKSDGLRGLOCGNNYS	180
Dh	122	GAGCATSLCFVYPLPFPARTPLAADVGR-RAOREFHGLDCDCKIKTFSKSDGLRGLOCGNNYS	180
Oy	180	VGGIJJYRAAYFCGVYDTAKGMLPDPKNVHIIYVSWMI AOSVTAAGVLGLSPEDTVRRRRMM	239
Dh	181	VGGIJJYRAAYFCGVYDTAKGMLPDPKNVHIIYVSWMI AOTVTAAGVLGLSPEDTVRRRRMM	240
Oy	240	OSGRKADIMYTGCTVDCMKRIAKDKGAKAFRFGAASNYLRMGGAFLVLYLDELKTKVY	297
Dh	241	OSGRKADIMYTGCTVDCMKRIAKDKGAKAFRFGAASNYLRMGGAFLVLYLDELKTKVY	298

RESULT 2
Q62164
ID Q62164 PRELIMINARY; PRT; 298 AA

DT 01-NOV-1996 (TREMblrel_01, Created)
DT 01-NOV-1996 (TREMblrel_01, Last sequence update)
DT 01-JUN-2002 (TREMblrel_21, Last annotation update)
DE Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar
DE to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide
DE translocator), member 4) (Hypothetical 32.9 kDa protein).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;

RC STRAIN-BALB/C; TISSUE=MUSCLE;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes.";

RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
CC INNER MEMBRANE (OI SIMILARITY).
DR EMBL; X74510: CAA52616.1: -.
DR EMBL; AF240002: AAF64470.1: -.
DR

DR InterPro: IPR002067; Mit carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR MGD: MGI:1353495; Slc25a4.
DR Ensembl: ENSG00000184120.5; LOC100289229.1.
DR Ensembl: ENSG00000184120.5; LOC100289229.1.

DR PRINIS; PRO0320; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Hypothetical protein; Inner membrane; Repeat; Transmembrane
 KW Transport; Mitochondrion.

SO SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match	94.28	Score 1463.5	DB 11	Length 298
Best Local Similarity	94.08	Pred. No. 7.7e-126		
Matches 280	Conservative 10	Mismatches 7	Indels 1	Gaps 1

Oy	1	MGHAAVSFLKDFLAGVNAANVAAKSTVAAPLERKLLLYOHAASKOISAEVKYKG11DCVVR	60
Oy	1	MGHAAVSFLKDFLAGVNAANVAAKSTVAAPLERKLLLYOHAASKOISAEVKYKG11DCVVR	60
Oy	1	MGHAAVSFLKDFLAGVNAANVAAKSTVAAPLERKLLLYOHAASKOISAEVKYKG11DCVVR	60
Oy	61	1PKEGFLSPFMRCLNANV1RYPTQALNFAFKDKYKQVFLGCVDRHHKQFMRYFAGNLASC	120
Oy	61	1PKEGFLSPFMRCLNANV1RYPTQALNFAFKDKYKQVFLGCVDRHHKQFMRYFAGNLASC	120
Oy	61	1PKEGFLSPFMRCLNANV1RYPTQALNFAFKDKYKQVFLGCVDRHHKQFMRYFAGNLASC	120
Oy	121	GAAGATSLCFVYPLDPAFRTRLAADVGR-RAQKEPFLGDC11K1FKSGDLGGLYCGFNVS	179
Oy	121	GAAGATSLCFVYPLDPAFRTRLAADVGR-RAQKEPFLGDC11K1FKSGDLGGLYCGFNVS	179
Oy	121	GAAGATSLCFVYPLDPAFRTRLAADVGR-RAQKEPFLGDC11K1FKSGDLGGLYCGFNVS	179
Oy	180	VQGI111YRAAYEGVDYTAGKMLPDPKNVH11FVSNM1AOSVTAVAGLSTPDDTVRRRRMM	239
Oy	181	VQGI111YRAAYEGVDYTAGKMLPDPKNVH11FVSNM1AOSVTAVAGLSTPDDTVRRRRMM	240
Oy	240	QSGRKAD1MYTCTVDCMKR1AKDEGAKAFYFGAASVNLBGMGAFVLYLDELTKKYV	297
Oy	241	QSGRKAD1MYTCTVDCMKR1AKDEGAKAFYFGAASVNLBGMGAFVLYLDELTKKYV	298
Oy	241	QSGRKAD1MYTCTVDCMKR1AKDEGAKAFYFGAASVNLBGMGAFVLYLDELTKKYV	298

RESULT 3	
Q8SQH5	
ID Q8SQH5	PRELIMINARY; PRT; 298 AA

DT 01-JUN-2002 (TremBurel 21, Created)
DT 01-JUN-2002 (TremBurel 21, last sequence update)
DT 01-JUN-2002 (TremBurel 21, last annotation update)
DE Adenine nucleotide translocator 2.

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional

DR EMBL: AB065433; BAB84673.1; -
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match	90.98	Score 1411.5	DB 6	Length 298
Best Local Similarity	89.98	Pred. No. 4.4e-121		
Matches 267	Conservative 16	Mismatches 13	Indels 1	Gaps 1

```

1 MTDAVSPAKDFLAGGVAALISKTAVAPIERVKLLLOVQHASKOITADKQYKGIIDCYR 60

```

Db 61 IPKEGVLSEWRGNLANVIRFPTQALNFAFKDKYQIFLGVDKRTQFMRYFAGNLASG 120

Oy 121 GAACATSLCEVYPLDPARTRLAADVGR-ADREFHIGDCIIKIFKSDGLRGLYOGFNV 179

180 VCGIIYRAYFGVYDTAKMLPDPKANVHIFVSMIAQSVTAVAGLLSYPEQTVRRRRMM 239

QY 240 QSGRRGADIMYTGTVDCMRRIAKDEGAKAFFKGAMSNVLRGNGAFVLYLDEIKKY 296
||||| :||||| :||||| :||||| :||||| :
DB 241 QSGRRGTDIMYTGTVDCMRRIARDEGAKAFFKGAMSNVLRGNGAFVLYLDEIKKF 297

RESULT 4	
09YIC4	
ID 09YIC4	PRELIMINARY; PRT: 298 AA.

```

AC 09YIC4:
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2002 (Tremblrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Neobatrachia: Ranioidea: Ranidae: Rana.
OX NCBI_TaxID=8410;
RN 111
RP MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
of a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36507.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carri. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match      88.7%: Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%: Pred. No. 5.7e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLLOVHASKOISAEKOYKGIIDCVR 60
DB 1 MTDNAISFAKDFLAGVAAVSKTAVAPIERVKLLLOVHASKOITADKOKGIMDCVVR 60
OY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 179
OY 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 180
OY 180 VOGIITRAAFVGYVDPAKGLPDPKKNVHIFVSMIAOSVAVAGLSTPYPTVRRRMM 239
DB 180 VOGIITRAAFVGYVDPAKGLPDPKKNVHIFVSMIAOSVAVAGLSTPYPTVRRRMM 239
OY 240 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 297
DB 240 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 297
OY 241 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 298
DB 241 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 298

RESULT 5
O9PRH1 PRELIMINARY: PRT: 298 AA.
ID O9PRH1:
AC O9PRH1:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Neobatrachia: Ranioidea: Ranidae: Rana.
OX NCBI_TaxID=8410;
RN 111
RP MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
of a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36507.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carri. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

```

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RT 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36513.1; -
DR EMBL: AB008456; BAA36506.1; -
DR EMBL: AB008461; BAA36511.1; -
DR EMBL: AB008462; BAA36512.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carri. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match      88.7%: Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%: Pred. No. 5.7e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLLOVHASKOISAEKOYKGIIDCVR 60
DB 1 MTDNAISFAKDFLAGVAAVSKTAVAPIERVKLLLOVHASKOITADKOKGIMDCVVR 60
OY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 179
OY 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADYGR-ADREFHGLGDCIYKFKSDGLGLYOGFNVS 180
OY 180 VOGIITRAAFVGYVDPAKGLPDPKKNVHIFVSMIAOSVAVAGLSTPYPTVRRRMM 239
DB 180 VOGIITRAAFVGYVDPAKGLPDPKKNVHIFVSMIAOSVAVAGLSTPYPTVRRRMM 239
OY 240 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 297
DB 240 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 297
OY 241 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 298
DB 241 QSGRRGADIMYTGVDCKRIAKDEGAKAFKFGAMSNVLRMGCAFVLVYLDEIKKYV 298

RESULT 6
O9PRH2 PRELIMINARY: PRT: 298 AA.
ID O9PRH2:
AC O9PRH2:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Neobatrachia: Ranioidea: Ranidae: Rana.
OX NCBI_TaxID=8410;
RN 111
RP MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
of a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36507.1; -
DR EMBL: AB008458; BAA36508.1; -
DR EMBL: AB008459; BAA36509.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.

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DR InterPro: IP0002030: Mit uncoupling.
DR Pfam: PF00153: mito. carr. 3
DR PRINTS: PR000926: MITOCARRIER.
DR PRINTS: PR00784: MTUOCCUPLING.
DR PROSITE: PS00215: MITOCH. CARRIER. 3.
DR Inner membrane: Mitochondrion; Transmembrane; Transport.
KW SEQUENCE 298 AA: 33082 MW: B0E225EB67599A06 CRC64:

Query Match	88.58;	Score 1374.5;	DB 13;	Length 298;
Best Local Similarity	86.28;	Pred. No. 1.1e-117;		
Matches 257;	Conservative 24;	Mismatches 16;	Indels 1;	Gaps 1.

[illegible]

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RESULT 7
ID      0919M9
AC      0919M9;      PRELIMINARY;      PRT;      298 AA.
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      Adenine nucleotide translocase.
GN      ANT1.
OS      Xenopus laevis (African clawed frog).
OC      Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Crawford M.J., Khosrowshahian F., Yarmuza S.L., Liversage R.A.;
RT      "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT      Dynamic Patterns of Expression During Development.";
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC      INNER MEMBRANE (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC      EMBL: AF21347; AAF63471.1;
DR      InterPro: IPR001993; MitoCh.carrler.
DR      InterPro: IPR002067; Mito.carrler.
DR      InterPro: IPR002030; Mlt.uncoupling.
DR      Pfam: PF00153; mltc.carr. 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PRINTS: PR00784; MTUNCOUPLING.
DR      PROSITE: PS00215; MITOCH_CARRIER. 3.
KW      Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE      298 AA; 32940 MW; 91BW7A0133751877F CRC64;

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	Query Match	88.0%	Score 1366.5;	DB 13;	Length 298;
	Best Local Similarity	86.2%;	Pred. No. 5,8e-117;		
	Matches 257; Conservative	23;	Mismatches 17;	Indels 1;	Gaps 1
OY	1	MGDHANSLKDLGAAVVAASKTVAPEERKKLLQVOHASKQISAETKYGIIDCVVR	60		

Db	1	MTDAAISFAKDFLAGGVAALISKTVAPIERVKLLLOVONHASKOTJADKHNGIMDCYVR	60
OY	61	IPKEGFLSPWBGNLANYRYEPTQALNEAFKDKYKQLEFLAGVDRIHKOFMRYFAGNLASG	120
Db	61	IPKEGFLSPWBGNLANYRYEPTQALNEAFKDKYKQLEFLAGVDRIHKOFMRYFAGNLASG	120
OY	121	GAAGTSLTCFVYPLDPARTRLAADVGRRA-QKEPFLGSCCIIKIFKSDCLRGLGYOFNNS	179
Db	121	GAAGTSLTCFVYPLDPARTRLAADVGRRA-QKEPFLGSCCIIKIFKSDCLRGLGYOFNNS	179
OY	180	VOGIIYRAAYFGVYDTAKGMLPDPKNVMI PYSMMIAQSVTAAGLSYFPDVRRRMM	239
Db	181	VOGIIYRAAYFGVYDTAKGMLPDPKNVMI PYSMMIAQSVTAAGLSYFPDVRRRMM	240
OY	240	OSGRGADIMTGTGVDCKRKIAKDECAKAFFGGANSNVLARGMGACVVLVLYDEIKKTY	297
Db	241	OSGRGADIMTGTGVDCKRKIAKDECAKAFFGGANSNVLARGMGACVVLVLYDEIKKTY	298

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RESULT 8
ID 095VX4 PRELIMINARY; PRT; 299 AA.
AC 095VX4;
DT 01-DEC-2001 (TREMBLrel_19, Created)
DT 01-DEC-2001 (TREMBLrel_19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel_20, Last annotation update)
DE ADP-ATP translocator.
OS Ethnostigmus rubripes.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda
OC Plurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostig
OX NCBI_TaxID=62613;
RN 11
RP SEQUENCE FROM N.A.
RA Burnell J.N.;
RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT rubripes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401758; ALA02100.1; -
DR EMBLpro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carrier.3.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SQ SEQUENCE 299 AA; 33037 MW; 3C3B8C46E7C3C5E CRC64;

```

Query Match	80.2%	Score 1245.5;	DB 5;	Length 299;
Best Local Similarity	80.3%	Pred. No. 7e-106;		
Matches 236; Conservative	25;	Mismatches 32;	Indels 1;	Gaps 1;

[illegible]

RESULT	9
Q9NHM5	
ID	Q9NHM5
AC	Q9NHM5;
DT	01-OCT-2000 (TREMBLrel, 15, Created)
	PRELIMINARY;
	PRT; 300 AA

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Drosophila; Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS MAL SEEKING;
 RA Chen Z., Pair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*."
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC EMBL: AF218587; AAF32322.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carrier.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 300 AA; 33036 MW; 5459DFOEAD0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;

Best Local Similarity 78.7%; Pred. No. 1.6e-105; Matches 236; Conservative 25; Mismatches 105; Indels 3; Gaps 1;

QY 1 MGDHA--WSFLKDFLAGAANAASKTAAVAPIERVKLLLOVQHASQISAEKQYKGIIDC 57
 DB 1 MCKEADPLGFKVDFPAAGGISAASVSTAAVAPIERVKLLLOVQHSISQISPDQYKGMIDC 60
 QY 58 VVRIPEQGFSLFWRGNLANVIRYPTQALNFAFKDKYKQLFGLGVDRHKQFRRFAGNI 117
 DB 61 FVRIPKEGFFASVWRGNMANVIRYPTQALNFAFKDKYKQVFLGVDRKNTQFRRYFLGNL 120
 QY 118 ASGGAAGATSLCFVYPLDFAKRLADVGRRAOREFHGDCDIKIFKSDGLGLYOGFN 177
 DB 121 ASGGAAGATSLCFVYPLDFAKRLADVGRRAOREFHGDCDIKIFKSDGLGLYOGFN 180
 QY 178 VSVQGIIRAAVFGYDTAKGMLPDPKNVHIFVSMIAQVSYAVAGLLSYPTDVRRRR 237
 DB 181 VSVQGIIRAAVFGYDTAKGMLPDPKNVHIFVSMIAQVSYAVAGLLSYPTDVRRRR 240
 QY 238 MMQSGRRGADIMYTGVCWRKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKKV 297
 DB 241 MMQSGRRGADIMYTGVCWRKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKKL 300

RESULT 10

095530

ID 095530

AC 095530

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)

DE 01-MAR-2002 (Tremblrel. 20, last annotation update)

DE GMI2886p (LP02726p).

GN SESB OR CG16944.

OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Stapleton M., Broksstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;

RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Broksstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez C., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celnik S.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 RC EMBL: AY060978; AAL28526.1;
 DR EMBL: AY070894; AAL48516.1;
 DR FLYBASE: FBgn0003360; SESB.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carrier.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN.3.
 SQ SEQUENCE 299 AA; 32909 MW; D51FE2A70BD59E8 CRC64;

Query Match 79.9%; Score 1241; DB 5; Length 299;

Best Local Similarity 79.7%; Pred. No. 1.8e-105; Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;

QY 5 ANSFLKDFLAGAANAASKTAAVAPIERVKLLLOVQHASQISAEKQYKGIIDCVRIPE 64
 DB 7 AVGFVKDFPAAGGISAASVSTAAVAPIERVKLLLOVQHSISQISPDQYKGMVDFIRIPE 66
 QY 65 OGFLFWRGNLANVIRYPTQALNFAFKDKYKQLFGLGVDRHKQFRRFAGNLSGGAAG 124
 DB 67 OGFLFWRGNLANVIRYPTQALNFAFKDKYKQVFLGVDRKNTQFRRYFLGNL 126
 QY 125 ATSLCFVYPLDFAKRLADVGRRAOREFHGDCDIKIFKSDGLGLYOGFN 184
 DB 127 ATSLCFVYPLDFAKRLADVGRRAOREFHGDCDIKIFKSDGLGLYOGFN 186
 QY 185 IYRAVFGYDTAKGMLPDPKNVHIFVSMIAQVSYAVAGLLSYPTDVRRRRMMQSGRK 244
 DB 187 IYRAVFGYDTAKGMLPDPKNVHIFVSMIAQVSYAVAGLLSYPTDVRRRRMMQSGRK 246
 QY 245 GADIMYTGVCWRKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKK 295
 DB 247 ATEVYIKNTLHCWATIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKK 297

RESULT 11

091336

ID 091336

AC 091336

DT 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-MAY-1999 (Tremblrel. 10, last sequence update)

DE 01-MAR-2002 (Tremblrel. 20, last annotation update)

DE ADP/ATP translocase.

OS Rana sylvatica (wood frog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=45438;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA MEDLINE-97398141; PubMed-9256066;

RA Cai O., Greenway S.C., Storey K.B.;

RT "Differential regulation of the mitochondrial ADP/ATP translocase gene

in wood frogs under freezing stress."

RL Biochim. Biophys. Acta 1353:69-78(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Cai O., Storey K.B.;

RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

CC -1- INNER MEMBRANE (BY SIMILARITY).

CC EMBL: U4832; AAA57882.2;

DR InterPro: IPR001993; Mitoch_carrier.

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DR InterPro: IPR002067; MitCarrier.
DR Pfam: PF00153; mito_carr. 3
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 317 AA; 35005 MW; 5F6B87ED8D5CEB72 CRC64;

Query Match 79.5%: Score 1234.5; DB 13; Length 317;
Best Local Similarity 85.7%: Pred. No. 7.6e-105;
Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 1 MGDIHASFLLKDFLAGAANAASKTAAPVPIERVKLLLOVONASKOISAEKQYKGIIDCVRIKPE 60
D 1 MTDANSPANDFLAGAAAMISKAAPVPIERVKLLLOVONASKOITADKQYKGIIDCVRIKPE 60
DB 1 PKEOGFLSEFWRCNLAVIRFPYQALNFGCKDKYKIFLDNDVKPTQFWRNRYFAGNLASG 120
OY 61 1PKEOGFLSEFWRCNLAVIRFPYQALNFAFKDKYKOLFLGCVDRHKQFWRNRYFAGNLASG 120
D 61 1PKEOGFLSEFWRCNLAVIRFPYQALNFGCKDKYKIFLDNDVKPTQFWRNRYFAGNLASG 120
OY 121 GAAGATSLCFYVPLDFAFRTLAADVGR-AQREHGLGDCILIKFKSDGLRGLYOGFNV 179
D 121 GAAGATSLCFYVPLDFAFRTLAADVGRKAGAREFNGLDCLAKIFKSDGLRGLYOGFNV 180
OY 180 VOGIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSYTAAGLSTYFPDTRRRMM 239
D 181 VOGIIRAAVFGVYDTAKGMLPDPKNTHIFVSMIAOSYTAAGFSGSYFPDTRRRMM 240
OY 240 OSGRKAGADIMYTGTCVDCMRKIAKDEGAKAFK 271
D 241 OSGRKAGAIMYSTGTCDCMKKIAIDEGGRAPFR 272

RESULT 12
O44093 PRELIMINARY: PRT: 288 AA.
ID 044093
AC 044093:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN 11
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
DR EMBL: AF025798; AAB87883.1; -.
DR FLYBase: FBgn0023292; Dpse/sesb.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31725 MW; 052B0CC005043680 CRC64;

Query Match 76.2%: Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%: Pred. No. 3.5e-100;
Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

OY 5 AMSFLKDFLAGAANAASKTAAPVPIERVKLLLOVONASKOISAEKQYKGIIDCVRIKPE 64
D 1 IIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSYTAAGLSTYFPDTRRRMMOSGRK 244
DB 7 AIGFVKDFAGGISAASKTAAPVPIERVKLLLOVONASKOISPDKQYKGVDFIRIPE 66
OY 65 OGFLSEFWRCNLAVIRFPYQALNFAFKDKYKOLFLGCVDRHKQFWRNRYFAGNLASGAG 124
D 67 OGFLSEFWRCNLAVIRFPYQALNFAFKDKYKOLFLGCVDRHKQFWRNRYFAGNLASGAG 126
OY 125 ATSLCFYVPLDFAFRTLAADVGRRAQREFGLDCLIKFKSGGLGLYOGFNV 184
D 127 ATSLCFYVPLDFAFRTLAADPTGKGQREFGLGNCILIKFKSDGLVGLYOGFNV 186
DB 187 IYRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSYTAAGLSTYFPDTRRRMMOSGRK 245
OY 245 GADIIMYTGTCVDCMRKIAKDEGAKAFKGAANSNLRGSGAFVLV 288
D 246 ATEIIVKNTLHCMTTIAKQCS-AFFKGAFSNLRGTGAFVLV 288

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D 67 OGFLSEFWRCNLAVIRFPYQALNFAFKDKYKOLFLGCVDRHKQFWRNRYFAGNLASGAG 126
OY 125 ATSLCFYVPLDFAFRTLAADVGRRAQREFGLDCLIKFKSGGLGLYOGFNV 184
D 127 ATSLCFYVPLDFAFRTLAADPTGKGQREFGLGNCILIKFKSDGLVGLYOGFNV 186
OY 185 IYRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSYTAAGLSTYFPDTRRRMMOSGRK 244
D 187 IYRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSYTAAGLSTYFPDTRRRMMOSGRK 245
OY 245 GADIIMYTGTCVDCMRKIAKDEGAKAFKGAANSNLRGSGAFVLV 288
D 246 ATEIIVKNTLHCMTTIAKQCS-AFFKGAFSNLRGTGAFVLV 288

RESULT 13
O44094 PRELIMINARY: PRT: 288 AA.
ID 044094
AC 044094:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN 11
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
DR EMBL: AF025799; AAB87884.1; -.
DR FLYBase: FBgn0023237; Dsub/sesb.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.2%: Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%: Pred. No. 3.5e-100;
Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

OY 5 AMSFLKDFLAGAANAASKTAAPVPIERVKLLLOVONASKOISAEKQYKGIIDCVRIKPE 64
D 7 AMGFVKDFAGGISAASKTAAPVPIERVKLLLOVONASKOISPDKQYKGVDFIRIPE 66
OY 65 OGFLSEFWRCNLAVIRFPYQALNFAFKDKYKOLFLGCVDRHKQFWRNRYFAGNLASGAG 124
D 67 OGFLSEFWRCNLAVIRFPYQALNFAFKDKYKOLFLGCVDRHKQFWRNRYFAGNLASGAG 126
OY 125 ATSLCFYVPLDFAFRTLAADVGRRAQREFGLDCLIKFKSGGLGLYOGFNV 184
D 127 ATSLCFYVPLDFAFRTLAADPTGKGQREFGLGNCILIKFKSDGLVGLYOGFNV 186
DB 187 IYRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSYTAAGLSTYFPDTRRRMMOSGRK 245
OY 245 GADIIMYTGTCVDCMRKIAKDEGAKAFKGAANSNLRGSGAFVLV 288
D 246 ATEIIVKNTLHCMTTIAKQCS-AFFKGAFSNLRGTGAFVLV 288

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RESULT 14
062526 PRELIMINARY: PRT: 307 AA.
AC 062526:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AN72 protein
CN AN72 OR CCG1683.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxId=7227;
EN 111
FP SEQUENCE FROM N.A.
FC STRAIN=BERKELEY;
FX MEDLINE=20196006; PubMed=10731132;
FA Adams M.D., Gelinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
FA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galie R.F.,
FA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
FA Sulton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
FA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
FA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
FA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
FA Bailei R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
FA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
FA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
FA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra J.,
FA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
FA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
FA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
FA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
FA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
FA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
FA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
FA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
FA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
FA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
FA Lasro P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
FA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
FA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
FA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
FA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
FA Palczolo M., Peltman G.S., Saunders R.D.C., Scheeler F., Shen H.,
FA Reiter K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
FA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
FA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
FA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
FA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
FA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
FA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
FA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT *The genome sequence of Drosophila melanogaster.*;
RL Science 287:2185-2195(2000).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RA Zhang Y.O., Davis A.W., Roote J., Ashburner M.;
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AE003484; AAF47956.1; -;
DR EMBL: Y10618; CAAT1629.1; -;
DR Flybase: FBgn0025111; Ant2.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlc_carrier.
DR Pfam: PF00153; mto_carr.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.
SQ SEQUENCE 307 AA: 33744 MW: 35633DPD82061CQC CRC64:

Query Match 73.9%; Score 1147; DB 5; Length 307;
Best Local Similarity 73.8%; Pred. No. 7.5e-97;

Matches 214; Conservative 33; Mismatches 43; Indels 7; Gaps 0;
QY 7 SFLKDFLAGVAAVAASKTRAVAPIEVKLLLOVONHASKOISAEKQYKGIIDCVVRIPKEOG 66
DB 17 SFLMDPMGVSAAIAKAVAPAEVKLLLOVONHASKOISAEKQYKGIIDCVVRIPKEOG 76
QY 67 FLSPFRGNLANVIRFPFOALNFAFKDKYKOLFGLGVDRHKOFPNFFAGNLSGCAAGAT 126
DB 77 FSSPFRGNLANVIRFPFOALNFAFKDKYKOLFGLGVDRHKOFPNFFAGNLSGCAAGAT 136
QY 127 SLGFVYPLDFARTRLAADVGRRAOREFHQGLDCIIRKFSQDGLRKYOGFNVSVGCI11Y 186
DB 137 SLGFVYPLDFARTRLAADVGRRAOREFHQGLDCIIRKFSQDGLRKYOGFNVSVGCI11Y 196
QY 187 RAAFGYVDATKAGLPDDKNVNIIPVSMIAOSVTVAVAGLLSPPTDVRRRMMOSGRCA 246
DB 197 RAAFGYVDATKAGLPDDKNVNIIPVSMIAOSVTVAVAGLLSPPTDVRRRMMOSGRCA 256
QY 247 DMYNYGTDCWKRIRAKDEGAKAFKFGAMSIVLRGAGFVLYDEIKKY 296
DB 257 EMVYNTAHCHLVIAKQEGTGAFFKALSNIIRGTGALLVLYLDEMKY 306
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AC 025129:
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DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase.
GN HRATLI.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxId=7729;
RN 111
RP SEQUENCE FROM N.A.
RA Miya T.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RA Miya T., Makabe K., Satoh N.;
RT *Expression of a gene for major mitochondrial protein, ADP/ATP
RT translocase, during embryogenesis in the ascidian Halocynthia
RT roretzi.*;
RL Dev. Growth Differ. 36:39-48(1994).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: D83069; BA011765.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlc_carrier.
DR Pfam: PF00153; mto_carr.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 304 AA: 33307 MW: 51FD0DD7D68634880 CRC64:

Query Match 73.4%; Score 1139.5; DB 5; Length 304;
Best Local Similarity 74.6%; Pred. No. 3.6e-96;
Matches 220; Conservative 18; Mismatches 54; Indels 3; Gaps 1;
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DB 3 WSADVFAKDLAIGCTAAAIKSTIVAPIEVKLLLOVONHASKOISAEKQYKGIIDCVVRIP 62
QY 63 KEQGFSLFRGNLANVIRFPFOALNFAFKDKYKOLFGLGVDRHKOFPNFFAGNLSGCA 122
DB 63 KEQGFSLFRGNLANVIRFPFOALNFAFKDKYKOLFGLGVDRHKOFPNFFAGNLSGCA 122
QY 123 AGATSLGFVYPLDFARTRLAADVGRRAOREFHQGLDCIIRKFSQDGLRKYOGFNVSVG 182
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Db	123	AGATGLCFVYPLDFARTRLADIGSGSRQFTGLGNCLATIVKKDGPRLYOGFVVSIOG	182
Oy	183	IIYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFDTVRRMMOSG	242
Db	183	IIYRAAYFGTIDTVKGMPLDPONPPIVSMIAQVVTGAGIISYPFDIVRRMMOSG	242
Oy	243	RKGADIMYGTVDGCMRKIAKDEGAKAFKGAWSNVLKMGCAFVLVLYDEIRKKYV	297
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Search completed: June 18, 2003, 13:36:01
 Job time : 83 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 02:39:09 : Search time 1656 Seconds

(without alignments)
15711.297 Million cell updates/sec

Title: US-09-393-441-1

Perfect score: 894

Sequence: 1 atgggtgatacgcctggag.....agatcaaaaaatgtctaa 894

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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12: gb_sy:*
13: gb_un:*
14: gb_vt:*
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16: em_fun:*
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18: em_in:*
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40: em_hlggo_mus:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Length	DB ID	Description
1	894	100.0	894	AX134718
2	894	100.0	894	AX301846
3	894	100.0	1320	9 HUMTRL
4	873	97.7	1319	BC008664
5	794.6	88.9	932	AB009386
6	770.6	86.2	1194	4 BOVT12TRANS
7	757.8	84.8	1196	6 AX401651
8	757.8	84.8	1196	10 RATANT1
9	751.4	84.0	1070	BC026925
10	751.4	84.0	1142	10 BC003791
11	748.2	83.7	1177	10 MMRNANC
12	748.2	83.7	1273	10 MMU27315
13	564.2	63.1	897	6 AX134720
14	564.2	63.1	897	6 AX301848
15	564.2	63.1	1399	9 BC031912
16	562.6	62.9	1193	9 BC008935
17	562.6	62.9	1308	9 BC007295
18	562.6	62.9	1344	9 AY007135
19	562.6	62.9	1366	9 BC007850
20	562.6	62.9	1455	9 BC014775
21	562.6	62.9	1466	9 BC008737
22	561	62.8	1146	4 AB065433
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25	554.4	62.0	1289	5 AF231347
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27	553	61.9	897	6 AX301847
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29	553	61.9	1228	9 HUMATPC
30	553	61.9	1236	10 BC004570
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32	553	61.9	1280	10 MMANTAP
33	548.2	61.3	1215	10 RATANT2
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44	528.8	59.1	183030	2 AC130772
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ALIGNMENTS

RESULT 1
AX134718
LOCUS AX134718 894 bp DNA linear PAT 29-MAY-2001
DEFINITION Sequence 1 from Patent WO0132876.
ACCESSION AX134718
VERSION AX134718.1 GI:14271235
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 894)
MURPHY/A.N., CLEVELANDER/W., WILLEY/S.E., ANDREYEV/A.Y., FRIGIERI/L.G.,
VELICHELBY/G. and DAVIS/R.E.
TITL Compositions and methods for determining interactions of


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Db 601 CTGCTGACCCCAAGAACGTGACATTTTGTGACGTGATGATTGCCCAAGTGTGACG 660
OY 661 GCACTCCAGGGCTGCTGCTCTACCCCTTTTGACACTGTTGCTGTAGATGATGACGAG 720
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OY 721 TCCGGCCGGAAGGGCCGATATATGATGACAGGGGACAGTTGACTGCTGGAGGAAGATT 780
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OY 841 ATGGGCGGTCTTTTGTATTGCTGTGTATGATGATGATCAAAAATATGCTTAA 894
Db 841 ATGGGCGGTCTTTTGTATTGCTGTGTATGATGATGATCAAAAATATGCTTAA 894

RESULT 3
LOCUS HUMTRL 1320 bp mRNA linear PRI 14-JAN-1995
DEFINITION Human mitochondrial ADP/ADP translocator mRNA, complete cds.
ACCESSION J02966
VERSION J02966.1 GI:339919
KEYWORDS ADP/ADP translocator.
SOURCE Human lower leg muscle, cDNA to mRNA, (library of Okayama-Berg),
clone pHMANT.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1320)
AUTHORS Neckelmann, N., Li, K., Wade, R.P., Shuster, R. and Wallace, D.C.
TITLE cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
of a leader peptide, divergence from a fibroblast translocator
cDNA, and coevolution with mitochondrial DNA genes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (21), 7580-7584 (1987)
MEDLINE 88041149
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by N. Neckelmann, 20-NOV-1987.
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Location/Qualifiers
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BASE COUNT 341 a 304 c 357 g 318 t
ORIGIN 102 bp upstream of NcoI site.

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Best Local Similarity 100.0% Pred. No. 31e-180:
Matches 894: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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OY 61 GTCTCCAGAGACCGCGGTGCGCCCATCAGAGAGGTCAAACTGCTGCTCAGCTCCAGCAT 120
Db 164 GTCTCCAGAGACCGCGGTGCGCCCATCAGAGAGGTCAAACTGCTGCTCAGCTCCAGCAT 223
OY 121 GCCAGCAACAGATCAGTCTGAGAGAGAGTACAAAGGATCATTGATTGCTGTGAGA 180
Db 224 GCCAGCAACAGATCAGTCTGAGAGAGAGTACAAAGGATCATTGATTGCTGTGAGA 283
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Db 284 ATCCCTAAGAGAGAGAGGCTTCTCTCTCTTCTGAGAGGGTAACTGCGCAAGCTATCCGT 343
OY 241 TACTTCCCAACCAAGCTCTCAACTTTCGCTTCAAGAGCAAGTACAGACAGCTTCTTCA 300
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Db 524 TTGGCTGCTGATGTGGGAGGCGGCGCCAGCGTGAATTCATGTGCTGGGCGACTGTATC 583
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Db 764 CCACTGCGAGGGCTGCTCTCTCTACCCCTTTTGACACTGTTGCTGCTGATGATGATGACG 823
OY 721 TCCGGCCGGAAGGGCCGATATTATGATACAGGGGACAGTTGACTGCTGGAGGAAGATT 780
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Db 884 GCAGAAAGACGAAGAGAGCCAGCCCTTCTTCAAGAGTGCCTGCTCAATGCTGAGAGGC 943
OY 841 ATGGGCGGTCTTTTGTATTGCTGTGTATGATGATGATCAAAAATATGCTTAA 894
Db 944 ATGGGCGGTCTTTTGTATTGCTGTGTATGATGATGATCAAAAATATGCTTAA 997

RESULT 4
LOCUS BC008664 1319 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, clone MGC:9281 IMAGE:3871960, mRNA, complete cds.
ACCESSION BC008664
VERSION BC008664.1 GI:14250453
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1319)
AUTHORS Strausberg, R.
```

TITLE Direct Submission
JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: villation@bcm.tmc.edu
 Villation, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRM Plate: 13 Row: K Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502096.
 Location/Qualifiers
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 /db_xref="taxon:9606"
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BASE COUNT 334 a 302 c 362 g 321 t
ORIGIN

Query Match 97.7%: Score 873; DB 9; Length 1319;
Best Local Similarity 99.1%: Pred. No. 9, 2e-176;
Matches 889; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

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 DB 99 ATGGGTATCACCCTTGAGACTTCTTAAGACTTCTTGCGCGGGCGGTGCGCGTGC 158
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 DB 219 GCCAGCAACAGATCATGCTGAGAGCAGTAACAAGGATCATTTGTTGTGTGAGAGA 278
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 OY 838 GGCATGCGCGGCTGCTTGTATGTGTGTGATGATGAGATCAAAAATATGTCTAA 894
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 DB 939 GGCATGCGCGGCTGCTTGTATGTGTGTGATGATGAGATCAAAAATATGTCTAA 995
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RESULT 5 932 bp mRNA linear MM 13-FEB-1999
 AB009386
 LOCUS
 DEFINITION
 ORYCTOLAGUS CUNICULUS mRNA for ADP/ATP translocase, complete cds.
 ACCESSION
 AB009386
 VERSION
 AB009386.1 GI:2668411
 KEYWORDS
 ADP/ATP translocase.
 SOURCE
 ORYCTOLAGUS CUNICULUS neonate male skeletal muscle cDNA to mRNA.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 1 (sites)
 Yamauchi, N. and Kasai, M.
 Identification of a 30kDa calsequestrin-binding protein, which regulates calcium release from sarcoplasmic reticulum of rabbit skeletal muscle
 JOURNAL
 1. Biochem. 335, 541-547 (1998)
 2 (bases 1 to 932)
 Yamauchi, N. and Kasai, M.
 Direct Submission
 TITLE
 Submitted (02-DEC-1997) Naohiro Yamauchi, Osaka University,
 Division of Biophysical Engineering, Machikaneyama 1-3, Toyonaka,
 Osaka 560, Japan (E-mail: n.yama@pe.es.osaka-u.ac.jp,
 Tel:+81-6-850-6542, Fax:+81-6-850-6557)
FEATURES
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 /organism="Oryctolagus cuniculus"
 /db_xref="taxon:9986"
 /sex="male"
 /tissue_type="skeletal muscle"
 /dev_stage="neonate"
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 /codon_start=1

[illegible]

LOCUS	BOVTITRANS	1194 bp	mRNA	linear	MM 12-AUG-1994
DEFINITION	Bovine ADP/ATP translocase T1 mRNA, complete cds.				
VERSION	M24102.1	JB81			
KEYWORDS	ADP/ATP translocase; translocase.				
SOURCE	Bos taurus cDNA to mRNA.				
ORGANISM	Bos taurus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.				
AUTHORS	1 (bases 1 to 1194)				
TITLE	Powell, S.J., Medd, S.M., Runswick, M.J. and Walker, J.E.				
JOURNAL	Two bovine genes for mitochondrial ADP/ATP translocase expressed				
MEDLINE	Biochemistry 28 (2), 866-873 (1989)				
PUBMED	89329093				
COMMENT	2540808				
FEATURES	On Aug 13, 1994 this sequence version replaced gi:341113.				
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	12..908				
	/note="The longest ORF is indicated.: T1"				
	/codon_start=1				
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	/db_xref="gi:529415"				
	/translation="MSDPAISFLKDLPLAGVAAAIISKTAAVPIERVKLLLOVHNASKRS				
	ISAKQVKKIICDCAVRIRPKEDGSLSPRGNIANYIRPPQALNPAFKDKKQIPLFG				
	VDRIKQWRPIRPNALASGAGATSLPEVYPLDRIARPLADYKGAARFETLGNIC				
	ITKTFKSDGLKGLYGFNVSVQGI11YRAAFGVYDTRAKGLPDPKNVH11VSMWIAQ				
	ITVTFAGLVASYFPDITVRMMDSGRKADIMYGTVDCKRK1AKDEGPKAFKFGANSH				
	NVLKMGCAFVLYVLDIKFV"				
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	1176..1181				
	polya_site				
	1194				
BASE COUNT	298 a 283 c 320 g 293 t				
ORIGIN					
Query Match	86.2%; Score 770.6; DB 4; Length 1194;				
Best Local Similarity	92.0%; Pred. No. 6e-154;				
Matches	825; Conservative 0; Mismatches 69; Indels 3; Gaps 1;				
1	ATGGGTGATCAGCGCTTGAGACCTTCCTTAAGACATTCCTGCGC86GCGTGGCGCTGCC 60				
2	ATGAGCGCATCAGGCGCTGTGAGCTTCCTGAAAGACATTCCTTGCGCGGCGTGGCGCTGCC 71				
3	GTCATCAGAACCGCGGTGCGCCCATCATGAGAGGCTCAACATCTGCTGACAGTCCAGCAT 120				
4	ATCTCCAAAGATCTGCTGTGCGCCCATCATGAGAGGCTCAACATCTGCTGACAGTCCAGCAT 131				
5	GCCAGCAACAGATCAGTGTGAGAGACAGTACAAAGGATCATTTGATGTGTGTGTGAGA 180				
6	GCCAGCAACAGATCAGTGTGAGAGACAGTACAAAGGATCATTTGATGTGTGTGTGAGA 191				
7	ATCCCTTAAGAGAGAGGCGCTTCCTGCTTCCTGAGAGGGTAACTGCGCAACAGTATCCGT 240				
8	ATCCCAAGAGAGAGGCGCTTCCTGCTTCCTGAGAGGGTAACTGCGCAACAGTATCCGT 251				
9	TACTTCCCAAGAGAGGCTTCCTGCTTCCTGAGAGGGTAACTGCGCAACAGTATCCGT 300				
10	TACTTCCCAAGAGAGGCTTCCTGCTTCCTGAGAGGGTAACTGCGCAACAGTATCCGT 311				
11	GGGGGTGTGATCGGATACGATTCGCGGCTACCTTGTGATTCGCGGCTGGCGGT 360				
12	GGGGGTGTGATCGGATACGATTCGCGGCTACCTTGTGATTCGCGGCTGGCGGT 371				

OY 361 GGGCGCGTGGGGCCACCTCCCTTTGCTTCTACCCCGTGCAGCTTTCAGAGCAGG 420
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LB 372 GGGCGACCTGGGGCCACCTCCCTTTGCTTCTACCCCGTGCAGCTTTCAGAGCAGG 431
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OY 421 TTGGCTGCTGATGTGGCGAGCG---GGCCAGCGGTATTCATGGTCTGGCGAGCTGT 477
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DB 432 CTGGCTGCCAGCTGGGGCGAAGGTGCCGCCAGCGGAGTTCACTGGTCTGGCACTGT 491
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OY 478 ATCATYCAAGATCTTCAAGTCTGATGGCTGAGGGGGCTTACAGGGTTTCAMAGCTCT 537
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DB 492 ATCACCAAGATCTTCAAGTCTGATGGCTGAGGGGGCTTACAGGGTTTCAGCTCTCG 551
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OY 538 GTCCAGGATCATATCTATAGAGTCCCTACTTGGAGTCTATGATCTGCCAGAGGG 597
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DB 552 GTCCAGGATCATATCTATAGAGTCCCTACTTGGAGTCTATGATCTGCCAGAGGG 611
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OY 598 ATGCTGCTGACCCCAAGAGCTGACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657
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DB 612 ATGCTGCTGACCCCAAGAGTGTGACATTTATGCTGAGCTGGATGATTTGCCAGAGTGTG 671
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OY 658 ACAGCACTCCAGAGGCTGCTGCTTACCCCTTTTGACACTGTTGCTGATGATGATG 717
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DB 672 ACAGCACTCCAGAGGCTGCTGCTTACCCCTTTTGACACTGTTGCTGATGATGATG 731
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OY 718 CAGTCCGCGGGAAGGGCGGATATATGATGACAGGGGACAGTGTGAGAGAG 777
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DB 732 CAGTCCGCGGGAAGGGCGGATATATGATGACAGGGGACAGTGTGAGAGAG 791
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OY 778 ATTCACAAAGACGAGAGGAGCCCTTCTTCMAAGTGGCTGCTCAATGTCTGAGA 837
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DB 792 ATTGCACAAAGATGAGAGCCCAAGCTTTCTTCAAGAGTGTCTGCTCAAGCTTACGA 851
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OY 838 GGCATGGCGGCTGCTTTTGTATGCTGCTTGTATGATGATGATGATGATGATGATG 894
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DB 852 GGCATGGCGGCTGCTTTTGTATGCTGCTTGTATGATGATGATGATGATGATGATG 908
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RESULT 7
AX401651 1196 bp DNA linear PAT 06-JUN-2002
LOCUS Sequence 1327 from Patent W00210453.
DEFINITION AX401651
ACCESSION AX401651
VERSION AX401651.1 GI:21337831
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and Elashoff,M.R.
TITLE Molecular toxicology modeling
JOURNAL Patent: WO 0210453-A 1327 07-FEB-2002;
Gene Logic, Inc. (US)
FEATURES
source location/Qualifiers
1..1196
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/note="EMBL/Genbank Accession No. D12770"

BASE COUNT 295 a 279 c 326 g 296 t
ORIGIN
Query Match 84.8% Score 757.8; DB 6; Length 1196;
Best Local Similarity 91.1% Pred. No. 3.2e-151;
Matches 817; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

OY 1 ATGGGTATACACCTTGAGACTTCTTAAGACTTCTGCGCGGGCGTCCGCTGCC 60
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DB 76 ATGGGGATCAGCTTGTGACTTCTTAAGACTTCTGCGAGGTGCTGCGCGCGCC 135
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OY 61 GTCTCCAAAGACCGCGTCCCGCATGACAGGATCAAACTGCTGCGAGGTCCAGCAT 120
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DB 136 GTCTCCAAAGACCGCGTCCCGCATGACAGGATCAAACTGCTGCGAGGTCCAGCAT 195
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OY 121 GCCAGCAAGACGATCAGTGTGAGAGCAGTACAAAGGATCATTTGATGTGTGAGA 180
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DB 196 GCCAGCAAGACGATCAGTGTGAGAGCAGTACAAAGGATCATTTGATGTGTGAGA 255
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OY 181 ATCCCTAAGAGCAGGCGTCTCTCTCTTCTGAGAGGGTAACTGGCCAACTGATCCGT 240
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DB 256 ATCCCAAGAGCAGGCGTCTCTCTCTTCTGAGAGGGTAACTGGCCAACTGATCCGG 315
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OY 241 TACTTCCCAAGCAGTCACTTCCCTTCAAGGACAGTCAAGCAGCTTCTTCTTA 300
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DB 316 TACTTCCCAAGCAGTCACTTCCCTTCAAGGACAGTCAAGCAGCTTCTTCTT 375
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OY 301 GCGGCTGTGATCGGCTTAAGCAGTCTTGCGGCTACTTGTGATGATGATGATGATG 360
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DB 376 GAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 435
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OY 361 GGGCGCTGAGGGCCACCTCCCTTTGCTTCTTACCCCGTGCAGCTTTCAGAGCAGG 420
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DB 436 GGGCGCTGAGGGCCACCTCCCTTTGCTTCTTACCCCGTGCAGCTTTCAGAGCAGG 495
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OY 421 TTGGCTGCTGATGAGGGCG---GGCCAGGTGATGATGATGATGATGATGATGATG 477
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DB 496 CTGGCTGCCAGCTGAGGAGGATCTTCCAGGATGATGATGATGATGATGATGATGATG 555
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OY 478 ATCATCAAGATCTTCAAGTGTGATGGCTGAGAGGGGCTTACAGGGTTTCAAGCTCT 537
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OY 538 GTCCAGGATCATATCTATAGAGTCCCTACTTGGAGTCTATGATGATGATGATGATG 597
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DB 616 GTGCAGGATCATATCTATAGAGTCCCTACTTCCAGGATCTATGACATGCGCAAGGG 675
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OY 598 ATGCTGCTGACCCCAAGAGCTGACATTTTGTGAGCTGATGATGATGATGATGATG 657
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DB 676 ATGCTGCTGACCCCAAGAGTGTGACATTTTGTGAGCTGATGATGATGATGATGATG 735
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OY 658 ACAGCACTCCAGAGGCTGCTGCTTACCCCTTTTGACACTGTTGCTGATGATGATGATG 717
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DB 736 ACAGCGTGGCGGGGCTGCTGCTTACCTTTCAGATTTGACACTGCTGCTGATGATGATG 795
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OY 718 CAGTCCGCGGGAAGGGCGGATATATGATGACAGGGGACAGTGTGAGAGAG 777
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DB 796 CAGTCCGCGGGAAGGGCGGATATATGATGACAGGGGACAGTGTGAGAGAG 855
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OY 778 ATTCACAAAGACGAGAGGAGCCCTTCTTCMAAGTGGCTGCTCAATGTCTGAGA 837
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DB 856 ATTCACAAAGATGAGAGCCCAAGCTTTCTTCAAGAGTGTCTGCTCAAGCTTACGA 915
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OY 838 GGCATGGCGGCTGCTTTTGTATGCTGCTTGTATGATGATGATGATGATGATGATG 894
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DB 916 GGCATGGCGGCTGCTTTTGTATGCTGCTTGTATGATGATGATGATGATGATGATG 972
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RESULT 8
RATANT1 1196 bp mRNA linear ROD 28-APR-2000
LOCUS Rattus norvegicus mRNA for mitochondrial adenine nucleotide
DEFINITION Rattus norvegicus
ACCESSION D12770.1 GI:398592
VERSION D12770.1
KEYWORDS adenine nucleotide translocator; isoform; mitochondrial inner
membrane protein; solute carrier.
SOURCE Rattus norvegicus (strain:Sprague-Dawley) cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1196)
AUTHORS Shinohara,Y., Kamida,M., Yamazaki,N. and Terada,H.
TITLE Isolation and characterization of cDNA clones and a genomic clone
encoding rat mitochondrial adenine nucleotide translocator

JOURNAL Biochim. Biophys. Acta 1152 (1), 192-196 (1993)
 MEDLINE 94002161
 REFERENCE
 AUTHORS
 TITLE
 Chemical, immunological, enzymatic, and genetic approaches to studying the arrangement of the peptide chain of the ADP/ATP carrier in the mitochondrial membrane
 JOURNAL
 MEDLINE
 REFERENCE
 AUTHORS
 TITLE
 Submitted (03-AUG-1992) Yasuo Shinohara, University of Tokushima, Tokushima 770, Japan (E-mail: yasuoe@tokushima-u.ac.jp, Tel: 81-886-33-7278, Fax: 81-886-33-5196)
 Submitted (03-AUG-1992) to DDBJ by: Yasuo Shinohara
 University of Tokushima
 Faculty of Pharmaceutical Sciences
 Tokushima 770
 Japan
 Phone: 0886-31-3111 x6255
 Fax: 0886-33-0510
 Location/Qualifiers
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 76. 972
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 BASE COUNT 295 a 279 c 326 g 296 t
 ORIGIN
 Query Match 84.8%; Score 757.8; DB 10; Length 1196;
 Best Local Similarity 91.1%; Pred. No. 3.2e-151;
 Matches 817; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

376 GGAGCTGTGATGTCATACAGCACTTCTGGCCCTACTTCCCTGTACCTGGCCTTCCT 435
 361 GGGGCGGCTGGGCGACCTCCCTTTGCTTTGCTACCGCGTGAATTTGTTAGACAGG 420
 436 GGGCGAGCTGGGGCTACTCCCTCTGCTTCTGCTACCACTGACATTTGCTAGACAGG 495
 421 TTGGCTGCTGATGTTGGGCGAGCG--CGCCAGCGCTGATTCATGCTGGGCGACTGT 477
 496 CTGGCTGCGAGCTGCGGACAGGAGATCTTCCAGCGCTGAGTTCAATGGCTGGTACTGT 555
 478 ATCATCAAGATCTTCAAGTCTGATGAGCTGACAGGGGCTCTACAGAGTTTCAAGTCTCT 537
 556 CTCACCAAGATCTTCAAGTCTGATGAGCTGAGAGGCTCTACAGAGTTTCAAGTCTCT 615
 538 GTCCAGGATCATATATATATAGAGCTGCTACTTGGAGCTATGATAGTCCAGAGGG 597
 616 GTGCGGCTATCATATATATATAGAGCTGCTACTTGGAGCTATGATAGTCCAGAGGG 675
 598 ATGCTGCTGACACCCCAAGACGTCGACATTTTGTGACCTGATGATTTGCCAGAGTGTG 657
 676 ATGCTGCGGACACCCCAAGATGTCACATTTATGTGACCTGATGATTTGCCAGAGTGTG 735
 658 ACGGAGTGCAGAGGCTGCTGCTTACCCCTTTGACACTGTTGCTGATAGATGATGATG 717
 736 ACAGCGCTGCGGGGCTGCTGCTTATCATATTTGACACTGCTGCTGATGATGATGATG 795
 718 CAGTCCGCGCGGAAGGGGCGGATTTATGATACAGGGGACACTGCTGCGAGGAG 777
 796 CAGTCTGCGGGAAGGGGCGGATTTATGATACAGGGGACACTGCTGCGAGGAG 855
 778 ATTGCAAGAGCAAGAGGAGGAGGAGGCTTTCTTCAAGAGGCTGCTGCTGATGATG 837
 856 ATTGCAAGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 915
 838 GGCATGGCGGCTGCTTTTGTATGTTGTTGATGATGATGATGATGATGATGATGATG 894
 916 GGCATGGCGGCTGCTTTTGTATGTTGTTGATGATGATGATGATGATGATGATGATG 972

RESULT 9
 BC026925
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (04-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRK Plate: 29 Row: f Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.

FEATURES

source

Location/Qualifiers

1..1070

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="MGC:25083 IMAGE:4500784"

/tissue_type="Eye, retina, mouse strain C57Bl/6"

/clone_lib="NIH_MGC_94"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

CDS

99..995

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/db_xref="GI:20070838"

/translation="MCDQALSLKPLAGIAAASKTAVAPIERVKLLQVYHASKO
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 VDRHKQFMRYFAGNLASGAGATSLCFVYPLDPTALADVGKSSOREFNGLDC
 LTKIFKSDGLKGYGFSVSGIIRAYFQVYDRAKMLDPKNNVHIVSNMIAO
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 NVLRMGGAIVLVLYDEIKKYV"

BASE COUNT 243 a 260 c 319 g 248 t

ORIGIN

Query Match 84.0%: Score 751.4; DB 10; Length 1070;

Best Local Similarity 90.6%: Pred. No. 7.4e-150;

Matches 813: Conservative 0; Mismatches 81; Indels 3; Gaps 1;

OY 1 ATGGGTGATCAGCGTTGGAGCTTCTTAAGAGACTTCCTGGCCGGGGCGTCCGCCCTGCC 60

DB 99 ATGGGGATCAGCGTTGAGCTTCTTAAGAGACTTCCTGGAGTGGAGTGGAGTGGAGTGG 158

OY 61 GTCTCCAGACCGCGGCGGCCCATCGAGAGAGGTCAAACTGCTGCGAGGTCCAGCAT 120

DB 159 GTCTCCAGACCGCGGCGGCCCATCGAGAGAGGTCAAACTGCTGCGAGGTCCAGCAT 218

OY 121 GCCAGCAACAGATCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

DB 219 GCCAGCAACAGATCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 278

OY 181 ATCCCTAAG 240

DB 279 ATCCCAAG 338

OY 241 TACTTCCCAAG 300

DB 339 TACTTCCCAAG 398

OY 301 GGGGCTGTGATGAG 360

DB 399 GGAAGGCTGTGATGAG 458

OY 361 GGGGCGGCTGGGGCAGCTTCTTGTCTTACCGGTGAGACTTGTGTAGAGCAGG 420

DB 459 GGGGCGGCTGGGGCAGCTTCTTGTCTTACCGGTGAGACTTGTGTAGAGCAGG 518

OY 421 TTGGGCTGTGATGAG 477

DB 519 CTGGCTGTGATGAG 578

OY 478 ATCATCAAGATCTTCAAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537

DB 579 CTCACCAAGATCTTCAAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638

OY 538 GTCCAGGATCATATTAATTAAGAGTCCCTTACCTGAGAGTCAATGATGATGATGATGAT 597

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OY 598 ATGCTGCTGATGAG 657

CDS

/product="Similar to solute carrier family 25

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DB 759 ACAGCGGTGGCGGCGCTGATGCTTACCGTTTGACACTTTGCTGCTGATGATGATGATG 818

OY 718 CACTCCGCGCGGAAGAGCGCGCATTTATGATACAGGAGGAGCACTTACCTGCTGAGAG 777

DB 819 CACTCTGCGCGCAAGAGCGCGCATTTATGATACAGGAGGAGCACTTACCTGCTGAGAG 878

OY 778 ATTCGAAAGAGCAAGAGAGCGCGCTTCTTAAGAGTCCCTGCTGCAATGCTGAGAG 837

DB 879 ATTCGAAAGAGCAAGAGAGCGCGCTTCTTCAAGAGTCCCTGCTGCAATGCTGAGAG 938

OY 838 GGCATGCGCGCTTCTTGTATTTGCTTATGATGATGATGATGATGATGATGATGATGATG 894

DB 939 GGCATGCGCGCTTCTTGTATTTGCTTATGATGATGATGATGATGATGATGATGATGATG 995

RESULT 10 1142 bp mRNA linear ROD 07-AUG-2002

BC003791 carrier:adenine nucleotide translocator, member 4, clone MGC:6027

LOCUS IMAGE:3599576, mRNA, complete cds.

DEFINITION BC003791.1 GI:13277809

ACCESSION BC003791

VERSION MGC.

KEYWORDS house mouse.

SOURCE Mus musculus.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 1142)

TITLE Strausberg, R.

JOURNAL Submitted (28-FEB-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) mdedpax11.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRK Plate: 11 Row: P Column: 4

This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF

analysis, Genescan gene prediction.

Location/Qualifiers

1..1142

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/db_xref="taxon:10090"

/map="FVB/N"

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/tissue_type="Mammary tumor, Metastatic lymph node, TGF alpha

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88..984

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 Oy 241 TACTTCCCAACCACTCTCAACTTCCCTTCAAGGACAGTACAGGAGCTCTCTCTTA 300
 Db 241 TACTTCCCAACCACTCTCAACTTCCCTTCAAGGACAGTACAGGAGCTCTCTCTTA 300
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 Db 301 GGGGGTGTGGATGCGATTAAGAGTCTGCGCTTACTTGGTGTAACTGGCTGCGGT 360
 Oy 361 GGGGGTGTGGATGCGATTAAGAGTCTGCGCTTACTTGGTGTAACTGGCTGCGGT 420
 Db 361 GGGGGTGTGGATGCGATTAAGAGTCTGCGCTTACTTGGTGTAACTGGCTGCGGT 420
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 Db 421 TTGGCTGTGATGTGGCAGG---CGGGCCAGCGTGAATTCATGCTGGGGCAGCTGT 477
 Oy 478 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGGGGCTTACAGGCTTCAAGCTCTCT 537
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 Oy 778 ATTGCAAAAGCAGAGGAGCAGGCTTCTTCAAGGCTGCTGAGTGAATGATGATG 837
 Db 781 ATTGCAAAAGCAGAGGAGCAGGCTTCTTCAAGGCTGCTGAGTGAATGATGATG 840
 Oy 838 GGCATGGCGGCTCTTTTGTATGCTGATGATGATGATGATGATGATGATGATGATG 894
 Db 841 GGCATGGCGGCTCTTTTGTATGCTGATGATGATGATGATGATGATGATGATGATG 897
 RESULT 15
 LOCUS BC031912 1399 bp mRNA linear PRI 26-JUN-2002
 DEFINITION Homo sapiens, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, clone MGC:29984
 IMAGE:5141625, mRNA, complete cds.
 ACCESSION BC031912
 VERSION BC031912.1 GI:21594692
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1399)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk

Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huljk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plate: 42 Row: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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 CDS
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 Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;
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 Db 38 ATGACGGAACAGAGCCATCTCTCCCAAGACTTCTTGGCCGAGGCAATCGCGCGGCC 97
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 Oy 121 GCCAGCAACAGATAGTGTGAGAGCAGTACAAAGGATCATTTGATGCTGTGAGAGA 180
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Db 398 GGTGGGGCCGGCCACCTCCCTTCCTCTTCGTGTACCCCTGGATTTTTCGCAACCCG 457

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Db 518 CTGGGAAGATATACCAGATCCGACGCAATCCGGGCTGTACCAGGGCTTCAAGTGTCTCC 577

538 GTCCAGGCACTATTATCTATAGAGCTGCCTACTTCCTGGAGTCTATATCTCGCAAGGG 597

Db 578 GTGCAGGGCATATCATCTACCGGGGCGGCTTACTTTCGGCTGTAGCATATAGGCCAAGGC 637

598 ATGTCGCTGACCCCAAGAACGTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657

638 ATGCTCCCGGACCCCAAGAACGCAATCGTGTGAGCTGGATGTATCGGCGAGACCGTG 697

Db 658 ACGGCAATGCGAAGGGCTGCTGTCTTACCCCTTTGACACTGTTCGTGTAGAAATGATGATG 717

698 ACGGCGCTGGCCGGCGGTGTCTTCAACCCCTTTCACAGCGGTGGGGGCGGCAAGATGATG 757

718 CAGTCCGGCCGGAAGAGCGCCGATATTATGTACAGCGGGGACAGTACTGCTGGAGGAAG 777

Db 758 CAGTCCGGCGCCGAAGAGCAATGACATCATGTACAGCGGCAACGCTGCACGTGTTGGAGSAG 817

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818 ATCTTCAGAGATGAGGGGGGCAAGGCCCTTCTTCAAGGGGCGGTGTCACACGTCCTGGG 877

838 GGCATATGGGGGCTTTTGTATTGCTGTGTATGATGAGATCAAAAAATATGTCTTA 894

878 GGCATATGGGGGCGCCCTTGTGCTGTGTATGATGAGACTCTCAAGAAAGGTGATCTTA 934

Search completed: June 22, 2003, 03:50:25
Job time : 1660 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 02:37:59 ; Search time 193 Seconds

(Without alignments)
10431.536 Million cell updates/sec

Title: US-09-393-441-1

Perfect score: 894
Sequence: 1 atgggtgacacgtctggag.....agatcaaaaatactgctaa 894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	894	100.0	894	21 AAD00519 Human adenine nucl
2	894	100.0	894	22 AAS05901 Human adenine nucl
3	894	100.0	894	24 AAS16688 DNA encoding human
4	757.8	84.8	1196	24 ABR63420 Rat sequence diffe
5	746.6	83.5	1259	19 AAV36480 Anti cDNA. Mus sp
6	745	83.3	1177	19 AAV36479 Ant1 cDNA. Mus sp
7	564.2	63.1	897	21 AAD00521 Human adenine nucl
8	564.2	63.1	897	22 AAS05903 Human adenine nucl
9	564.2	63.1	897	24 AAS16690 DNA encoding human

C	10	562.6	62.9	1212	22	AA158797	Human polynucleoti
C	11	562.6	62.9	2035	22	AA160583	Human polynucleoti
C	12	553	61.9	897	21	AAD00520	Human adenine nucl
C	13	553	61.9	897	24	AAS05902	Human adenine nucl
C	14	553	61.9	897	24	AAS16689	DNA encoding human
C	15	523.2	58.5	1156	23	AAS91243	DNA encoding novel
C	16	503.6	56.3	1581	23	ABL18511	Drosophila melanog
C	17	503.6	56.3	1750	23	ABL20967	Drosophila melanog
C	18	488	54.6	1116	24	ABK3761	Human cDNA differe
C	19	488	54.6	1116	24	ABN95598	Gene #2096 used to
C	20	488	54.6	1116	24	ABL69347	Prostate cancer re
C	21	473	52.9	5768	24	ABL61797	Colon adenocarcino
C	22	451.2	50.5	2706	22	AAS29836	Human cytoskeletal
C	23	451.2	50.5	2706	22	AAS35083	DNA #33 encoding h
C	24	451.2	50.5	220895	24	ABK64788	Human cDNA differe
C	25	446	49.9	853	24	AAS61966	Porcine muscular s
C	26	443.2	49.6	1033	23	ABL03127	Drosophila melanog
C	27	434.6	48.6	788	24	AAS61967	Porcine muscular s
C	28	407	45.5	453	22	ABL24495	Human breast cancer
C	29	398.6	44.6	687	24	ABO56282	Human ovarian anti
C	30	371	41.5	1781	24	AAD33664	Human TRICH-19 cDN
C	31	362.6	40.6	1251	23	AAS79610	DNA encoding novel
C	32	346.8	38.8	4545	23	AAS68190	DNA encoding novel
C	33	330.8	37.0	5407	23	ABL18510	Drosophila melanog
C	34	330.8	37.0	8031	23	ABL20966	Drosophila melanog
C	35	292.6	32.7	707	21	AAAN01634	Human colon cancer
C	36	290	32.4	501	24	AAS61620	Lung small cell ca
C	37	277.8	31.1	943	24	ABN74319	Bovine embryonic g
C	38	271.8	30.4	520	22	AA115651	Bovine breast cancer
C	39	249	27.9	988	24	ABN74435	Bovine embryonic g
C	40	241.6	27.0	464	22	ABA42741	Human breast cell
C	41	241.6	27.0	464	22	ABA53168	Human foetal liver
C	42	241.6	27.0	464	22	ABA22942	Probe #1408 for ge
C	43	241.6	27.0	464	22	AAK01416	Human brain expres
C	44	241.6	27.0	464	22	AAK26867	Human bone marrow
C	45	241.6	27.0	464	22	AA111497	Probe #1430 for ge

ALIGNMENTS

RESULT 1	AAD00519	standard; cDNA: 894 BP.
ID	AAD00519	
XX	XX	
AC	AAD00519:	
XX	XX	
DT	29-AUG-2000	(first entry)
XX	XX	
DE	Human adenine nucleotide translocator ANTI cDNA.	**
XX	XX	
KW	Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;	
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MP; cancer;	
KW	mitochondrial permeability transition; neuroprotective; neurotrophic;	
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	antiproliferative; cerebroprotective; therapeutic; screening; psoriasis;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW	diabetes; Leber's hereditary optic neuropathy; lactic acidosis; stroke; MIDD;	
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;	
KW	myoclonic epilepsy red ragged fibre syndrome; ss.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FT	Key	Location/Qualifiers
FT	CDS	1..894
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PD	11-MAY-2000.	
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PF 03-NOV-1999; 99WO-US25883.
 XX 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR:
 PI Ghosh SS:
 DR MPI: 2000-365619/31.
 P-PSDB: AAV71031.
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX
 PS Example 1: Page 165; 175pp: English.

CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is a cDNA
 CC encoding adenine nucleotide translocator ANT1 from human brain.
 XX
 SO Sequence 894 BP; 187 A; 224 C; 267 G; 216 T; 0 other:

Query Match 100.0%; Score 894; DB 21; Length 894;
 Best Local Similarity 100.0%; Pred. No. 2e-248;
 Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 ATGGGTGATCAGCGCTTGAGAGCTTCTTAAGCACTTCTGCGGGGGCGCTGCCCTGCC 60
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 OY 541 CAAGCATCATTAATCTATAGAGCTGCTCTTCCGAGAGCTATGATACCAAGGGATG 600
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 DB 781 GCAAAAGACGAAAGGACCAAGCGCTTCTTCAAGGTGCTGTCATGCTGAGAGCGC 840
 OY 841 ATGGCGGTGCTTTTGTATGCTTGTATGATGATGATGATCAAAATAATATGCTAA 894
 DB 841 ATGGCGGTGCTTTTGTATGCTTGTATGATGATGATGATCAAAATAATATGCTAA 894

RESULT 2

AA05901 ID AAS05901 standard; cDNA: 894 BP.

AA05901:

07-SEP-2001 (first entry)

Human adenine nucleotide translocator-1 (ANT-1) cDNA sequence.

Human: adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 mitochondrial permeability transition pore component; cell survival;
 mitochondrial core component; mitochondrial related disorder; cancer;
 Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 1..897

FT /*tag= a

FT /product= "ANT-1"

MO200132876-A2.

10-MAY-2001.

03-NOV-2000; 2000WO-US30535.

03-NOV-1999; 99US-0434354.

(MITO-) MITOKOR.

Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;

Velicelebi G, Davis RE;

MPI: 2001-291054/30.

P-PSDB: AAV01198.

New nucleic acid expression constructs, useful for screening for agents
 that alter mitochondrial permeability transition (MPT), comprises
 polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 fused to energy transfer molecule -

XX PS Disclosure; Fig 1: 186pp; English.
 XX CC The present sequence encodes for human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX CC
 S2 Sequence 894 BP: 187 A; 224 C; 267 G; 216 T; 0 other:

Query Match 100.0%; Score 894; DB 22; Length 894;
 Best Local Similarity 100.0%; Pred. No. 2e-248;
 Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGGGATATCAGCGCTTGGAGCTTCTTAAGAGCTTCCGGCGGGGGGGTGGCGGCC 60
 1 ATGGGATATCAGCGCTTGGAGCTTCTTAAGAGCTTCCGGCGGGGGGGTGGCGGCC 60
 61 GTCTCAAGAGCCGGGTCGCCCATCGAGAGGTCAGTCTGTCGACAGTCCAGCAT 120
 61 GTCTCAAGAGCCGGGTCGCCCATCGAGAGGTCAGTCTGTCGACAGTCCAGCAT 120
 61 GTCTCAAGAGCCGGGTCGCCCATCGAGAGGTCAGTCTGTCGACAGTCCAGCAT 120
 121 GCCAGCAAGAGATCACTGCTGAGAGAGCAGTCAAGAGGATGATTTGTTGTGTGAGA 180
 121 GCCAGCAAGAGATCACTGCTGAGAGAGCAGTCAAGAGGATGATTTGTTGTGTGAGA 180
 181 ATCCCTAAGAGAGAGGCTTCCCTCTGAGAGGGTAACTGGGCAAGATGATCCGT 240
 181 ATCCCTAAGAGAGAGGCTTCCCTCTGAGAGGGTAACTGGGCAAGATGATCCGT 240
 181 ATCCCTAAGAGAGAGGCTTCCCTCTGAGAGGGTAACTGGGCAAGATGATCCGT 240
 241 TACTTCCCAAGAGAGGCTTCCCTCTGAGAGGGTAACTGGGCAAGATGATCCGT 300
 241 TACTTCCCAAGAGAGGCTTCCCTCTGAGAGGGTAACTGGGCAAGATGATCCGT 300
 241 TACTTCCCAAGAGAGGCTTCCCTCTGAGAGGGTAACTGGGCAAGATGATCCGT 300
 301 GGGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 360
 301 GGGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 360
 301 GGGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 360
 361 GGGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 420
 361 GGGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 420
 361 GGGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 420
 421 TTGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 480
 421 TTGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 480
 421 TTGGCTGTGATGCGGATAGCACTTTGCGCTACTTTGCTGTAACCTGGCTCCGCT 480
 481 ATCAAGATCTTCAAGTCTGATGGCTGAGGGGCTTCAACAGGGTTTCAACGCTCTGTC 540
 481 ATCAAGATCTTCAAGTCTGATGGCTGAGGGGCTTCAACAGGGTTTCAACGCTCTGTC 540
 481 ATCAAGATCTTCAAGTCTGATGGCTGAGGGGCTTCAACAGGGTTTCAACGCTCTGTC 540
 541 CAAGGATCATTTATCTATAGAGCTGCTACTTGGAGTCTATGATGCTGCAAGGGGATG 600
 541 CAAGGATCATTTATCTATAGAGCTGCTACTTGGAGTCTATGATGCTGCAAGGGGATG 600
 541 CAAGGATCATTTATCTATAGAGCTGCTACTTGGAGTCTATGATGCTGCAAGGGGATG 600
 601 CTGCTGACCCCAAGAGAGCTGACATTTTGTGAGCTGATGATTTGCCAAGAGTGTGACG 660
 601 CTGCTGACCCCAAGAGAGCTGACATTTTGTGAGCTGATGATTTGCCAAGAGTGTGACG 660

661 GCACTGCGAGGCTGCTGCTTACCCCTTTGACACACTGTGCTGACAGATGATGATGACG 720
 661 GCACTGCGAGGCTGCTGCTTACCCCTTTGACACACTGTGCTGATGATGATGATGACG 720
 721 TCCGCGCGGAGAGGGGCGGATATATATATATATATATATATATATATATATATAT 780
 721 TCCGCGCGGAGAGGGGCGGATATATATATATATATATATATATATATATATATAT 780
 721 TCCGCGCGGAGAGGGGCGGATATATATATATATATATATATATATATATATATAT 780
 781 GCAAG 840
 781 GCAAG 840
 841 ATGGGCGGCTGCTTTGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 900
 841 ATGGGCGGCTGCTTTGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 900
 RESULT 3
 ID AAS16688 standard; CDNA: 894 BP.
 XX AAS16688;
 XX AAS16688;
 XX 14-FEB-2002 (first entry)
 DE DNA encoding human adenine nucleotide translocator 1 (ANT1).
 XX Human; adenine nucleotide translocator; ANT; ss;
 KW mitochondrial matrix protein.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 1..894
 FT /tag= a
 FT /product= "Adenine nucleotide translocator 1 (ANT1)"
 XX WO200185944-A2.
 XX 15-NOV-2001.
 XX 11-MAY-2001; 2001WO-US15416.
 XX 11-MAY-2000; 2000US-0569327.
 XX (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK; **
 XX WPI: 2002-055598/07.
 DR P-PSDB: MAU10378.
 XX Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 PS
 PS Example 1; Fig 1; 147pp; English.
 XX The invention relates to a recombinant expression construct (1)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesized in the mitochondrial
 CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (1) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-

CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the coding sequence of human ANTI.
 XX
 XX
 XX Sequence 894 BP; 187 A; 224 C; 267 G; 216 T; 0 other;

Query Match 100.0%; Score 894; DB 24; Length 894;
 Best Local Similarity 100.0%; Pred. No. 2e-248;
 Matches 894: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ATGGGTGATCAGCTTGGAGCTTCTTAAAGACTTCTGGCCGGGGCGGCTGCC 60
    |||||||
DB 1 ATGGGTGATCAGCTTGGAGCTTCTTAAAGACTTCTGGCCGGGGCGGCTGCC 60
OY 61 GTCTCCAGAGCCGGGTGCGCCCATCGAGAGGCTCAAACTCTCTGTCAGTCCAGCAT 120
    |||||||
DB 61 GTCTCCAGAGCCGGGTGCGCCCATCGAGAGGCTCAAACTCTCTGTCAGTCCAGCAT 120
OY 121 GCCAGCAACAGATGAGTGTGAGAGGCTCAAAAGGATGATGATGTTGTGTGAGCA 180
    |||||||
DB 121 GCCAGCAACAGATGAGTGTGAGAGGCTCAAAAGGATGATGATGTTGTGTGAGCA 180
OY 181 ATCCCTAAGAGAGAGGGCTTCTCTCTCTGAGAGGGGTAACTGGCCAACTGATCCGT 240
    |||||||
DB 181 ATCCCTAAGAGAGAGGGCTTCTCTCTCTGAGAGGGGTAACTGGCCAACTGATCCGT 240
OY 241 TACTTCCCAACCAAGCTCTCACTTGGCTTCAAGAGACAGTACAGAGCTCTTCTTA 300
    |||||||
DB 241 TACTTCCCAACCAAGCTCTCACTTGGCTTCAAGAGACAGTACAGAGCTCTTCTTA 300
OY 301 GGGGGTGTGGATCGGATTAAGAGATTTGGCGCTTGTGTTGTTGTTGTTGTTGTTGTT 360
    |||||||
DB 301 GGGGGTGTGGATCGGATTAAGAGATTTGGCGCTTGTGTTGTTGTTGTTGTTGTTGTT 360
OY 361 GGGGGCGGTGGGGACCACTCCCTTGTCTTGTCTACCCCGCTGAGCTTGTCTGAGACAG 420
    |||||||
DB 361 GGGGGCGGTGGGGACCACTCCCTTGTCTTGTCTACCCCGCTGAGCTTGTCTGAGACAG 420
OY 421 TTGGCTGTGATGTGGGAGGCGCCGACGCTGAGTTCCATGCTGTGGGCACTGTATC 480
    |||||||
DB 421 TTGGCTGTGATGTGGGAGGCGCCGACGCTGAGTTCCATGCTGTGGGCACTGTATC 480
OY 481 ATCAAGATCTTCAAGTCTGATGCGCTGAGAGGGGCTCTACAGGGTTTCAAGCTCTCTC 540
    |||||||
DB 481 ATCAAGATCTTCAAGTCTGATGCGCTGAGAGGGGCTCTACAGGGTTTCAAGCTCTCTC 540
OY 541 CAAGGCATCATTTATCTATGAGCTGCTTCTCGAGTCTATGATACCTCCCAAGGGGATG 600
    |||||||
DB 541 CAAGGCATCATTTATCTATGAGCTGCTTCTCGAGTCTATGATACCTCCCAAGGGGATG 600
OY 601 CTGCTGAGCCCAAGAACGTCACATTTTGTGAGCTGTGATGTTGCCAGAGTGTGAGC 660
    |||||||
DB 601 CTGCTGAGCCCAAGAACGTCACATTTTGTGAGCTGTGATGTTGCCAGAGTGTGAGC 660
OY 661 CGAGTTCGAGGGGCTCTGCTTCAACCCCTTGTGACACTGTTGCTGCTGAGATGATGCG 720
    |||||||
DB 661 CGAGTTCGAGGGGCTCTGCTTCAACCCCTTGTGACACTGTTGCTGCTGAGATGATGCG 720
OY 721 TCCGCCCGGAAAGGGGCGCATATTTATGACAGGGGAGAGTGTGAGTGTGAGTGTGAG 780
    |||||||
DB 721 TCCGCCCGGAAAGGGGCGCATATTTATGACAGGGGAGAGTGTGAGTGTGAGTGTGAG 780
OY 781 GCAAAAGAGAGAGAGCCCAAGGCTTCTTCAAAAGTGTGCTGAGAGAGC 840
    |||||||
DB 781 GCAAAAGAGAGAGAGCCCAAGGCTTCTTCAAAAGTGTGCTGAGAGAGC 840
OY 841 ATGGGGGCTGCTTTGTATGTTGTATGATGATCAAAATATCTCTAA 894
    |||||||
DB 841 ATGGGGGCTGCTTTGTATGTTGTATGATGATCAAAATATCTCTAA 894
  
```

RESULT 4
 ABK63420

ID ABK63420 standard; cDNA; 1196 BP.
 AC ABK63420;
 DT 18-JUN-2002 (first entry)
 DE Rat sequence differentially expressed in response to a hepatotoxin #1327.
 XX Rat: ss: hepatotoxin; expressed sequence tag: EST; drug screening;
 XX differential expression; centrilobular necrosis; steatosis.
 XX Rattus norvegicus.
 PN WO200210453-A2.
 XX
 XX 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US23872.
 XX
 PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-290029P.
 PR 15-MAY-2001; 2001US-290645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-295798P.
 PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 P1 WPI: 2002-241625/29.
 XX
 DR Predicting toxic effects of compounds or the progression of these toxic
 XX effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells -
 PS
 XX
 PS Claim 1: Seq ID No 1327; 239pp; English.
 XX
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilize a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.
 XX

Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 other;

Query Match 84.8% Score 757.8; DB 24; Length 1196;
Best Local Similarity 91.1% Pred. No. 5.8e-209;
Matches 810; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

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OY 1 ATGGGTATCATACGCTTGAGCTTCTCTTAAGAGACTTCTGGCGCGGCGCGCTGCC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 ATGGGGATCAGAGCTTTGAGCTTCTCTTAAGAGACTTCTGGCGAGTGGCAGTCCGCC 135

OY 61 GTCTCAAGACCGCGGTCCGCCCTGAGAGGCTCAAACTGCTGTCAGAGTCCAGCAT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 GTCTCAAGACCGCGGTCCGCCCTGAGAGGCTCAAACTGCTGTCAGAGTCCAGCAT 195

OY 121 GCCAGCAAGAGATCACTGCTGAGAGACAGTACAAAGGATCATTTGATGTGTGTAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 GCCAGCAAGAGATCACTGCTGAGAGACAGTACAAAGGATCATTTGATGTGTGTAGA 255

OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGCTTAACCTGGCCAACTGATCCGT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGCTTAACCTGGCCAACTGATCCGT 315

OY 241 TACTTCCCAACCCCAAGCTTCACACTTCCCTTCAAGAGACAAAGTCAAGCAGCTCTCTTA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 TACTTCCCAACCCCAAGCTTCACACTTCCCTTCAAGAGACAAAGTCAAGCAGATCTTCTGTG 375

OY 301 GGGGCTGTGATCGGCATTAAGCAAGTTCGGCGCTACTTGTGTGTAACCTGCGCTCCGCT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 376 GGAGGTGTGATCTCTCATTAAGCAAGTTCGGCGCTACTTGTGTGTAACCTGCGCTCCGCT 435

OY 361 GGGGCGCTGGGCGCAGCTCCCTTGTGTGTGTAACCGCGGACTTGTGTGTAAGACAGG 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 436 GGGGCGCTGGGCGCAGCTCCCTTGTGTGTGTAACCGCGGACTTGTGTGTAAGACAGG 495

OY 421 TTGGCTCTGATGTGGCAGGCG--CGCCAGCGTGAATTCCTGCTGTGGCGAGCTGT 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 496 CTGGCTGCGCAGCGTGGCGAAGGATCTCCAGCGTGAATTCCTGCTGTGGCGAGCTGT 555

OY 478 ATCATCAAGATCTTCAAGTGTGATGCGCTGAGGGGCTCTACACAGGCTTTCACGCTCTCT 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 556 CTCACCAAGATCTTCAAGTGTGATGCGCTGAGGGGCTCTACACAGGCTTTCACGCTCTCT 615

OY 538 GTCCAGAGGATCATTAATCTATAGAGTGGCTACTTCCGAGTCTATGATACGCCAAGGGG 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 616 GTCCAGAGGATCATTAATCTATAGAGTGGCTACTTCCGAGTCTATGATACGCCAAGGGG 675

OY 598 ATGCTGCTGACCCCAAGAGAGTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 676 ATGCTGCTGACCCCAAGAGAGTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 735

OY 658 ACGGCACTCGCAGGCGTGTCTCTTACCCCTTGCACACTGTTCTGTAGATGATGATG 717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 ACACCGCTGCGCGGCTGTGTCTCTATTCATCTTACACTGCTCCCTGTAGATGATGATG 795

OY 718 CAGTCCGCGCGGAAGGGCGGATATATATACACGGGAGAGTGTGATGATGAGAGAG 777
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 796 CAGTCCGCGCGGAAGGGCGGATATATATACACGGGAGAGTGTGATGATGAGAGAG 855

OY 778 ATTCAAAAGAGAGAGAGAGAGAGGCTTCTTCAAAAGTGCCTGCTCAAAAGTCTGAGA 837
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 856 ATTCAAAAGAGAGAGAGAGAGAGGCTTCTTCAAAAGTGCCTGCTCAAAAGTCTGAGA 915

OY 838 GGCATGGCGGCTGCTTTTGTATGTGTGTGTATGATGATCAAAATAATGTCTAA 894
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 916 GGCATGGCGGCTGCTTTTGTATGTGTGTGTATGATGATCAAAATAATGTCTAA 972

```

RESULT 5
AAV36480
10 AAV36480 standard; DNA: 1259 BP.

XX AAV36480;
XX

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DT 28-SEP-1998 (first entry)
XX
DE Ant1 cDNA.
XX
KW Ant1; Adenine nucleotide translocator; cloning; screening;
KW DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fascioclular muscular dystrophy;
KW lactic acidosis; degenerative muscle disease; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 190..1086
    /tag= a
    /product= "Ant1 protein"
XX
PN M09819714-A1.
XX
PD 14-MAY-1998.
XX
PF 31-OCT-1997; 97WO-US19882.
XX
PR 01-NOV-1996; 96US-0030017.
XX
PA (UYEM-) UNIV EMORY.
XX
P1 Graham BC, Macgregor GR, Wallace DC;
XX
DR WP1: 1998-286608/25.
XX
PT Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
PS Disclosure; Page 40; 61pp; English.
XX
XX The present sequence is a mouse Ant1 degenerate cDNA sequence, cloned
CC by screening a mouse heart cDNA library with the human Ant1 cDNA as a
CC probe. The Ant1 cDNA sequence was determined by DNA Taq dideoxy
CC terminator cycle sequencing. The Ant1 protein is encoded by the Ant1
CC locus, a nuclear gene on chromosome 8. This protein is required in
CC mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which
CC can then be converted into ATP. An Ant1 homozygous mutant would thus be
CC defective in OXPHOS which results in disease in oxidative metabolism
CC dependent tissues. This mouse Ant1 homozygous mutant can be used as a
CC model system for fascioclular muscular dystrophy, hypertrophic
CC cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can
CC be used to test possible therapeutic compounds which increase/mediate ATP
CC and ADP exchange across the mitochondrial membrane independent of Ant1.
XX
XX
SO Sequence 1259 BP; 274 A; 311 C; 339 G; 269 T; 66 other;

```

Query Match 83.5% Score 746.6; DB 19; Length 1259;
Best Local Similarity 90.3% Pred. No. 1e-205;
Matches 810; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

```

OY 1 ATGGGTATCATACGCTTGAGCTTCTCTTAAGAGACTTCTGGCGCGGCGCTGCC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 ATGGGGATCAGAGCTTTGAGCTTCTCTTAAGAGACTTCTGGCGAGTGGCAGTCCGCC 249

OY 61 GTCTCAAGACCGCGGTCCGCCCTGAGAGGCTCAAACTGCTGTCAGAGTCCAGCAT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 GTCTCAAGACCGCGGTCCGCCCTGAGAGGCTCAAACTGCTGTCAGAGTCCAGCAT 309

OY 121 GCCAGCAAGAGATCACTGCTGAGAGACAGTACAAAGGATCATTTGATGTGTGTAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 310 GCCAGCAAGAGATCACTGCTGAGAGACAGTACAAAGGATCATTTGATGTGTGTAGA 369

OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGCTTAACCTGCGCAAGCTGATCCGT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 370 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGCTTAACCTGCGCAAGCTGATCCGT 429

```

OY	241	TACATTCGCCACCACCAAGCTCTCAACTCTCCCTTCAAGGACAGTACACAGACTCTTCTTA	300
Db	430	TACTTCCCTCCACTCAAGCCCTCAACTGCCCTTCAAAAGATACACACATCTTCTCG	489
OY	301	GGGGGTGTGAGATCGGCAATAGACAGTTCTGGGGGCTACTTTCGGTGAACCTGGCGCGGT	360
Db	490	GGAGGCGTGGATCCGCATTAAGCAGTTCTGGGGCTACTTTCGGTGAACCTGGCGCTTGGT	549
OY	361	GGGGCGCGTGGGGCCACCCTCCCTTTCCTTTGCTCTAACCCGCTGACCTTTCCTAGNCCAGG	420
Db	550	CGGGAGCTGGGGGCCACCTCCCTCTGCTTTCGCTACACCCGCTGGACTTTCCTAGGAGCCAGG	609
OY	421	TTGGCTGCTGATGTGGGAGAGCG---CGCCCAAGCGTGACTTCATGCTCTGGCGCATCTGT	477
Db	610	CTGGCTGGCGAGCTGGGGGCAAGGAGATCTTCCAGCGAGAAATTCATTAAGGGCTGGCGCATGT	669
OY	478	ATCATCAAGATCTTCAAGTCTGATGGAGCGCTGAAGGGGCTCTACAGGGTTTCAGGCTCTCT	537
Db	670	CTCACCAAGATCTTCAAGTCCGAGCGGCTTGAGAGGGTCTCTACAGGGTTTCAGTGTCTCT	729
OY	538	GTCCAAGGCATTCATTATATAGAGCTCCCTACTTCGGAGTCTATGATACATGCCAAGGGG	597
Db	730	GTCAGAGGCTATCATCATCTACAGAGCTGCTACTTCGGAGTCTATGACACTGCCAAGGGG	789
OY	598	ATGGCGCCCTGAGCCCAAGAGAGTGGACATTTTTCGGAGCTGGATGATGCCAAGGCTGTG	657
Db	790	ATGCTGCCAGACCCCAAGAAATGTGCATATTAATCTGAGCTGGATGATATGCCAGAGTGTG	849
OY	658	ACGGCAGTTCGAGAGGCTGCTGCTCCATCCCTTTTGACAGTGTTCGTCGTAGATGATGATG	717
Db	850	ACAACGGTGGGGGGCTGTGTGCTATCCGTTTGACACTGTTCGTCGTAGATGATGATG	909
OY	718	CAGTTCGGCCCGGAAGGGCGGATATTAATGTAACAGGGGACAGTTGACTGCTGAGAGAG	777
Db	910	CAGTCTGCCCGCAAAAGGGCTGATATTAATGTAACAGGGGACACTTGACTGCTGAGAGAG	969
OY	778	ATTGCAAAAGACGAAGAGAGCCAGGCCCTTCTTCAAAAGGTGGCTGCCAATGTGCTAGAG	837
Db	970	ATTGCAAAAGATGAAGAGAGCCACCCCTTCTTCAAAAGGTGCTGCTGCCAATGTGCTAGAG	1029
OY	838	GGCATGGCGGCTGCTTTTGTATTTGCTGTTGTATGATGATGATCAAAAAATATGCTCTAA	894
Db	1030	GGCATGGCGGCTGCTTTTGTATTTGCTGTTGTATGATGATGATCAAAAAATATGCTCTAA	1086
RESULT 6			
AAV36479			
XX	ID	AAV36479 standard: DNA: 1177 BP.	
XX	AC		
XX	AAV36479:		
XX	28-SEP-1998	(first entry)	
XX	DE	Anl1 cDNA.	
XX	KW	Anl1: Adenine nucleotide translocator: cloning; screening:	
XX	KW	DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation:	
XX	KW	probe: OXPHOS: mitochondria; ADP: ATP: homozygous mutant; myopathy:	
XX	KW	hypertrrophic cardiomyopathy; fascioscapular humeral muscular dystrophy:	
XX	XX	lactic acidosis; degenerative muscle disease; ss.	
XX	OS	Mus sp.	
XX	Key	Location/Qualifiers	
XX	FT	94...990	
XX	FT	/tag= a	
XX	FT	/product= "Anl1 protein"	
XX	PD	WO9819714-A1.	
XX	PD	14-MAY-1998.	

[illegible]

OY 538 GTCCAGGACATCATTTATATAGAGTCCCTACTTGGAGTGTATGATGACCCAGGG 597
 DB 634 GTCCAGGACATCATCTACAGAGTCCCTACTTGGAGTGTATGATGACCCAGGG 693
 OY 598 ATGCTGCTGACCCCAAGACGTCACATTTTGTAGAGTGTATGATGACCCAGGTG 657
 DB 694 ATGCTGCTGACCCCAAGACGTCACATTTTGTAGAGTGTATGATGACCCAGGTG 753
 OY 658 ACGGACGTGCGAGGGCTGCTGTCTTACCCCTTTGACACTGTTCTGTAGATGATG 717
 DB 754 ACACGCTGTGCGGGCTGTGTCTTATCCGTTTACACTGTTCTGTAGATGATG 813
 OY 718 CAGTCCGCGCGGAAGGGCGGATATATGATGACGGGAGAGTGTGATGAGAG 777
 DB 814 CAGTCTGCGCGGAAGGGCGGATATATGATGACGGGAGAGTGTGATGAGAG 873
 OY 778 ATTCGAAAGAGAGGAGGAGCCCTTCTTCAAGAGTGTGCTGCAATGTCTGAGA 837
 DB 874 ATTCGAAAGAGAGGAGGAGCCCTTCTTCAAGAGTGTGCTGCAATGTCTGAGA 933
 OY 838 GGCATGGGCGGCTGTTTGTATGATGATGATGATGATGATGATGATGATG 894
 DB 934 GGCATGGGCGGCTGTTTGTATGATGATGATGATGATGATGATGATGATG 990

RESULT 7

AAD00521 standard: cDNA: 897 BP.

AAD00521:

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT3 cDNA.

Human: adenine nucleotide translocator; ANT3; mitochondria; ADP: ATP; adenosine triphosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; neurologic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antipsychotic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome; ss.

Homo sapiens.

Location/Qualifiers

1..897

/tag= a

/product= "ANT3"

MO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99WO-US25883.

03-NOV-1998; 98US-0185904.

08-SEP-1999; 99US-0334441.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;

Ghosh SS;

WP1: 2000-365619/31.

P-PSDB: AAY71033.

Recombinant construct encoding adenine nucleotide translocator

polypeptide, useful e.g. in screening for potential therapeutic agents

PT against mitochondrial disease -
 XX
 PS Example 1: Page 166: 175pp: English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is a cDNA
 CC encoding adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SO Sequence 897 BP: 174 A: 274 C: 287 G: 162 T: 0 other:

Query Match 63.1%: Score 564.2: DB 21: Length 897:

Best Local Similarity 77.6%: Pred. No. 5.5e-153:

Matches 696: Conservative 0: Mismatches 198: Indels 3: Gaps 1:

OY 1 ATGGGATGATCAGCTGAGCTCTTCAAGAGCTTCTGCGCGGCGGCTGCGCTGCC 60
 DB 1 ATGAGGACAGACGATCTCTTCCGCAAGAGCTTCTGCGCGGAGGACATGCGCGCC 60
 OY 61 GTCTCCAGAGCCGGGTGCGCCCGCCAGAGGCTCAACTGCTGTCGACAGTCCACAT 120
 DB 61 ATCTCAAGAGCGCGCTGCGCTCCAGTACGAGCGGCTCAAGCTGCTGACAGTCCAC 120
 OY 121 GCCAGCAAGAGATCACTGCTGAGAACAGCAGTCAAGAGGATGATGATGATGATG 180
 DB 121 GCCAGCAAGAGATGCGCGCGGACAGCAGTCAAGAGGATGATGATGATGATGATG 180
 OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTTCTGAGAGGCTTAACCTGAGCAGTATCGCT 240
 DB 181 ATCCCAAGAGAGAGGCTTCTCTCTTCTGAGAGGCTTAACCTGAGCAGTATCGCT 240
 OY 241 TACTTCCCAAGAGCTTCACTTGCCTTCAAGAGCAAGTCAAGAGCAGCTTCTTA 300
 DB 241 TACTTCCCAAGAGCTTCACTTGCCTTCAAGAGCAAGTCAAGAGCAGCTTCTTA 300
 OY 301 GGGGCTGATGCGGATGAGCAGTCTGCGGCTGATGCTGTAACCTGAGCTGCGGCT 360
 DB 301 GGGGCTGATGCGGATGAGCAGTCTGCGGCTGATGCTGTAACCTGAGCTGCGGCT 360
 OY 361 GGGGCGCTGGGCGACCTGCTTGTGCTTGTACCGGCTGAGCTTGTGAGCAGCAGG 420
 DB 361 GGGGCGCTGGGCGACCTGCTTGTGCTTGTGAGCAGCAGGCTTGTGAGCAGCAGG 420
 OY 421 TTGCTGCTGATGAGGAGG--CGCGCCAGGCTGAGTTCATGCTGAGGAGCTGT 477
 DB 421 TTGCTGCTGATGAGGAGG--CGCGCCAGGCTGAGTTCATGCTGAGGAGCTGT 477
 OY 478 ATCATCAAGATCTTCAAGTGTGATGAGGCTGAGGAGGCTGATGAGGAGGCTGAT 537
 DB 478 ATCATCAAGATCTTCAAGTGTGATGAGGCTGAGGAGGCTGATGAGGAGGCTGAT 537
 OY 538 GTCCAGGACATCATTTATATAGAGTCCCTACTTGGAGTGTATGATGATGATGATG 597
 DB 538 GTCCAGGACATCATCTACAGAGTCCCTACTTGGAGTGTATGATGATGATGATG 597
 OY 541 GTCCAGGACATCATCTACAGAGTCCCTACTTGGAGTGTATGATGATGATGATG 600
 DB 541 GTCCAGGACATCATCTACAGAGTCCCTACTTGGAGTGTATGATGATGATGATG 600
 OY 598 ATGCTGCTGACCCCAAGACGTCACATTTTGTAGAGTGTATGATGATGATGATG 657
 DB 598 ATGCTGCTGACCCCAAGACGTCACATTTTGTAGAGTGTATGATGATGATGATG 657
 OY 601 ATGCTGCTGACCCCAAGACGTCACATCTGCTGAGTGTATGATGATGATGATG 660
 DB 601 ATGCTGCTGACCCCAAGACGTCACATCTGCTGAGTGTATGATGATGATGATG 660
 OY 658 ACGGACGTGCGAGGGCTGCTGTCTTACCCCTTTGACACTGTTCTGTAGATGATGATG 717

[illegible]

Query Match	Best Local Similarity	Score	DB 22	Length	897
Matches	696	Conservative	0	Mismatches	198
				Indels	3
				Gaps	1
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					0 other
63.1%	Score	564.2	DB 22	Length	897
77.6%	Pred.	No. 5,5e-153			
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1	ATGACGGAAACAGCGCCATCTCTTCCCAAAGCTTTGCGCGGAGCGATCCCGCCCGCC	60			
61	GTCCTCAAGACCGCGCGTGCAGCCCAATCAGAGGCTCAAACTGCTCTGACGCTCCAGCAT	120			
61	ATCTCCAAAGACCGCGGTGCTCCAGTCCAGCGCGGTCAAGCTCTCTGACGCTCCAGCAT	120			
121	GCCAGCAAAACAGATCAGTCTGAGAGCAGTCAAAAGGATCATTTGTTGTGTGACA	180			
121	GCCAGCAAAACAGATGCGCGCGCGACAGAGCATCAAGGGCATCTGGACATTTGTCCGC	180			
181	ATCCCTAAGAGGACGAGGCTGCTCTCTCTCTTGGAGGGGTAACTCTGGCAAGCATACCGT	240			
181	ATCCCAAGAGGACGAGGCTGCTCTCTCTTGGAGGGGTAACTCTGGCAAGCATACCGT	240			
241	TACTTCCCAACAGCTCTCAACTTGCCTTCAAGGACAGCAAGTACAGACGCTCTTCTTAA	300			
241	TACTTCCCAACAGCTCTCAACTTGCCTTCAAGGATTAAGTACAGACGATCTTCTG	300			
301	GGGGGTGTGATCGGCATTAAGCAGTTCGTGGCGCTACTTGTGTGAACCTGGCGTCCGT	360			
301	GGGGGTGTGATCGGCATTAAGCAGTTCGTGAAGTACTTGTGGCGGCAACCTGGCGTCCGT	360			
361	GGGGGTGTGAGGACGCTCTCTCTTGTCTCAAGGCTGAGCTTTGTGTGAGCAGG	420			
361	GGGGGTGTGAGGACGCTCTCTCTTGTCTCAAGGCTGAGCTTTGTGTGAGCAGG	420			
421	TTGGCTGTGATGTGGCAGG--CGCGCCACAGCTGATGATTCATGTGTGTGGCGCATGT	477			
421	TTGGCTGTGATGTGGCAGG--CGCGCCACAGCTGATGATTCATGTGTGTGGCGCATGT	477			
478	ATCATCAAGATCTTCAAGCTGATGATGAGGCGGCGTCTACAGAGGTTTCAAGCTCTCT	537			
478	ATCATCAAGATCTTCAAGCTGATGATGAGGCGGCGTCTACAGAGGTTTCAAGCTCTCT	537			
538	GTCCAAAGCATATCTATATAGAGCTCTCTACTTTCGGAAGTATAGTACTGCAAGAGG	597			
538	GTCCAAAGCATATCTATATAGAGCTCTCTACTTTCGGAAGTATAGTACTGCAAGAGG	597			
541	GTCCAAAGCATATCTATACCGGCGGCTACTTCCGCGGTGTAGATACGCGCAAGGCG	600			
541	GTCCAAAGCATATCTATACCGGCGGCTACTTCCGCGGTGTAGATACGCGCAAGGCG	600			
558	ATGCTGCTGACCCCAAGACAGTGTGACATTTTGTGAGCTGATGATATGCCAGAGGTG	657			
558	ATGCTGCTGACCCCAAGACAGTGTGAGCTGATGATGATGATGATGATGATGATGATG	657			
601	ATGCTGCTGACCCCAAGACAGTGTGAGCTGATGATGATGATGATGATGATGATGATG	660			
601	ATGCTGCTGACCCCAAGACAGTGTGAGCTGATGATGATGATGATGATGATGATGATG	660			
658	ACGCGAGTGTGAGGCTGCTGCTCAAGCTCTTGTGACATGTTTGTGCTGAGATGATGATG	717			
658	ACGCGAGTGTGAGGCTGCTGCTCAAGCTCTTGTGACATGTTTGTGCTGAGATGATGATG	717			
661	ACGCGAGTGTGAGGCTGCTGCTCAAGCTCTTGTGACATGTTTGTGCTGAGATGATGATG	720			
661	ACGCGAGTGTGAGGCTGCTGCTCAAGCTCTTGTGACATGTTTGTGCTGAGATGATGATG	720			
718	CAGTCCGCGCGGAAAGGCGGATATTTATGTAACAGGCGGACAGTTGACTGCTGAGAG	777			
718	CAGTCCGCGCGGAAAGGCGGATATTTATGTAACAGGCGGACAGTTGACTGCTGAGAG	777			
721	CAGTCCGCGCGGAAAGGCGGATATTTATGTAACAGGCGGACAGTTGACTGCTGAGAG	780			
721	CAGTCCGCGCGGAAAGGCGGATATTTATGTAACAGGCGGACAGTTGACTGCTGAGAG	780			
778	ATTTCAAGATGAGGCGGCAAGCGCTTTCTTCAAGGGTGGCTGCTCCAGCTCTCGCG	837			
778	ATTTCAAGATGAGGCGGCAAGCGCTTTCTTCAAGGGTGGCTGCTCCAGCTCTCGCG	837			
781	ATTTCAAGATGAGGCGGCAAGCGCTTTCTTCAAGGGTGGCTGCTCCAGCTCTCGCG	840			
781	ATTTCAAGATGAGGCGGCAAGCGCTTTCTTCAAGGGTGGCTGCTCCAGCTCTCGCG	840			
838	GGCATGGGCGGCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	894			
838	GGCATGGGCGGCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	894			
841	GGCATGGGCGGCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	897			
841	GGCATGGGCGGCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	897			

OS Homo sapiens.
 XX PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US34263.
 XX PR 21-JAN-2000; 2000US-0488725.
 XX PR 25-APR-2000; 2000US-0552317.
 XX PR 09-JUL-2000; 2000US-0598042.
 XX PR 19-JUL-2000; 2000US-0620312.
 XX PR 03-SEP-2000; 2000US-0653450.
 XX PR 14-SEP-2000; 2000US-0652191.
 XX PR 19-OCT-2000; 2000US-0693036.
 XX PR 29-NOV-2000; 2000US-0727344.
 XX PA (HYSE-) HYSEQ INC.
 XX P1 Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 P1 Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
 P1 Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX DR WPI: 2001-442253/47.
 XX DR P-PSDB; AAM39641.
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries.
 XX PS Claim 1: SEQ ID NO 1000; 10078bp; English.
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX SO Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 other;
 Query Match 62.9%; Score 562.6; DB 22; Length 1212;
 Best Local Similarity 77.5%; Pred. No. 1.8e-152;
 Matches 695; Conservative 0; Mismatches 199; Indels 3; Gaps 1;
 OY 1 ATGGGTGATCAGCGCTTGAGAGCTTCTTAAGAGACTTCCTGCGGGGCGGTCCCGCTGCC 60
 DB 131 ATGACGGAACAGCGCATCTCTCTTCCGCAAGACTTCTTGGCCGAGGCAATCCCGCGCC 190
 OY 61 GTCTCCAGACCGCGGTCCGCCCATCGAGAGGCTCAAACTCTGCTGCAGCTCCAGCAT 120
 DB 191 ATCTCCAGACGGCGGTGCTCGATCGAGCGGTCAACCTCTGCTGAGGTCCAGCAC 250
 OY 121 GCCAGCAACAGATCATGCTCTGAGAGAGCATACAAAGGATCATTTGCTGTGAGA 180
 DB 251 GCCAGCAACAGATCATGCTCTGAGAGAGCATACAAAGGATCATTTGCTGTGAGA 310
 OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTCTCTGAGAGGAGTAACCTGGCCCAAGCTATCGCT 240
 DB 311 ATCCCTAAGAGAGAGGCTTCTCTCTCTCTGAGAGGAGTAACCTGGCCCAAGCTATCGCT 370
 OY 241 TACTTCCCAACCAAGCTCTCAACTTCTGCTTCAAGGAGACATACAAAGGAGCTTCTT 300
 DB 371 TACTTCCCAACCAAGCTCTCAACTTCTGCTTCAAGGAGACATACAAAGGAGCTTCTT 430

OY 301 GGGCGGTGATGATGAGCATTAAGCACTTCTTCCGCTACTTTCCTGCTATACCTGGCGCCGT 360
 DB 431 GGGGCGGTGAGCAACACACAGCATTTCTGAGACTTTCGCGGCAACCTGGCGCCGTCCGCG 490
 OY 361 GGGGCGGTGAGCGACACCTCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCT 420
 DB 491 GGTGCGCGCGCGGCGACCT 550
 OY 421 TTGGCTGCTGATGTGGCAGG--CGCGCGCGCGCTGAGTTCATGCTGTGGCGACTGT 477
 DB 551 CTGGCAGCGGAGCTGGAAGAGTCAGGACAGAGCGCGGAGTTCGAGGCGCTGGAGACTGC 610
 OY 478 ATCATCAAGATTTTAAGTCTATGAGGCTGAGAGGCGCTTACCAGGGTTTCAAGCTTCT 537
 DB 611 CTGGTGAAGATCACCAAGTCGACGCGCATCCGCGGCTCTGTACAGGGCTTCAAGTCTTC 670
 OY 538 GTCCAAAGCATATTATCTATGAGCTGCTACTTTCGAGTCTATGATACCTCCAAAGGG 597
 DB 671 GTGCAAGGATCATATCATCTACCGCGGCTTACTTCTGCGGTATGAGATACGCGCAAGGGC 730
 OY 598 ATGCTGCTGACCCCGCAAGACGTGCATTTTGTGAGCTGTGATATTCGCCAGAGTGTG 657
 DB 731 ATGCTGCCCGGACCCCAAGACGACATCGTGTGAGCTGTGATGATGCGCGCAAGCCGTG 790
 OY 658 ACGGCACTGCGAGGCGCTCTCTTACCCCTTTGACACTGTTCCTGTAAGATGATGATG 717
 DB 791 ACGGCGGTGCGCGGCTGTGCTTACCCCTTTCGACACGCGTCCGCGCGGCGATGATGATG 850
 OY 718 CAGTCCGCGGGAAGGGCGCATTTATGTACAGGCGAGCACTTGACGTGCGGAGGAG 777
 DB 851 CAGTCCGCGGGAAGGAGGCTGACATCATGTAACAGGCGACCTGCGACTGTGGAGGAAG 910
 OY 778 ATTGCAAAAGAGCAAGAGGAGGAGGCTTCTTCAAGAGTCCCTGCTCAATGTCTGAGA 837
 DB 911 ATCTTCAGAGATGAGGCGGCGCAAGGCTTCTTCAAGGAGTCCGCTGCTCAAGCTCTCGGG 970
 OY 838 GCGATGCGCGCTCTTTTGTATGCTGTGTATGATGATGATGATGATGATGATGATGATG 894
 DB 971 GCGATGCGCGCGCTCTTTTGTATGCTGTGTATGATGATGATGATGATGATGATGATGATG 1027
 RESULT 11
 AA160583/c
 ID AA160583 standard; cDNA: 2035 BP.
 AC AA160583;
 XX
 DT 22-OCT-2001 (first entry)
 XX DE Human polynucleotide SEQ ID NO 4572.
 XX KW Human; neurotrophic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX KW Homo sapiens.
 XX PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US34263.
 XX PR 21-JAN-2000; 2000US-0488725.
 XX PR 25-APR-2000; 2000US-0552317.
 XX PR 09-JUL-2000; 2000US-0598042.
 XX PR 19-JUL-2000; 2000US-0620312.
 XX PR 03-AUG-2000; 2000US-0653450.
 XX PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000: 2000US-0693036.
 PR 29-NOV-2000: 2000US-0727344.
 XX (HYSE-) HYSEO INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;
 DR WPI: 2001-442253/47.
 DR P-PSDB: AAM41427.
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 XX Claim 1: SEQ ID NO 4572; 10078bp; English.
 XX
 XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemoclastic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 XX Sequence 2035 BP: 398 A: 611 C: 625 G: 401 T: 0 other:
 SO
 Query Match 62.9% Score 562.6; DB 22; Length 2035;
 Best Local Similarity 77.5% Pred. No. 2.3e-152;
 Matches 695; Conservative 0; Mismatches 199; Indels 3; Gaps 1;
 Oy 1 ATGGGTCATCAGCCCTTGAGACTTCTTAAAGACTTCTTGCGCGCGGCGTCCGCCGCC 60
 Db 1932 ATGACGAGAACAGGCGCATCTCTTCCGCAAGAACTTCTTGCGCGCGGCGTCCGCCGCC 1873
 Oy 61 GTCTCCAGACCCCGGTCGCCCCATCAGAGAGGTCMAACTCTGCTGACAGTCCACAT 120
 Db 1872 ATCTCCAAAGAGCGCGGCTCGATCGAGCGGTCMAAGCTGCTGCTGACAGTCCACAC 1813
 Oy 121 GCCAGCAAAAGATCACTGCTGAGAACCACTACAAAGGATCATTTGTCGTGAGA 180
 Db 1812 GCCAGCAAGAGATCGCGCGCAACAGCACTACAAAGGATCATTTGTCGTGCGC 1753
 Oy 181 ATCCCTAAGAGAGAGGCTTCTCTCTTCTTGAGAGGATTAACCTGCGCAAGTATCGT 240
 Db 1752 ATCCCAAGAGAGAGGCGCTGCTCTCTTCTTGAGAGGCAACCTTGCCAAAGTATTCGC 1693
 Oy 241 TACTTCCCAACCAAGCTCTCAACTTCGCTTCAAGAGACATACAAAGAGCTTCTTGA 300
 Db 1692 TACTTCCCAACCAAGCTCTCAACTTCGCTTCAAGAGATTAAGATACAAAGAGATCTCTG 1633
 Oy 301 GGGGCTGTGATGGGCTATAGCACTTCTGCGCTACTTCTGTAACCTGCGGCTCGGT 360
 Db 1632 GGGGCGCTGTGAGCAAGCAACAGCTTCTGAGAGTATTTGCGGCAACCTGCGGCTCGGC 1573
 Oy 361 GGGGCGCTGTGAGGCAACCTCTCTTCTTGTCTTACTCCGCTGACCTTGTGATAGACAGG 420
 Db 1572 GTGCGCGCGCGCGGCACTCTCTCTCTGCTGTGATACCGCTGATTTTCCGCAAGACCGGC 1513
 Oy 421 TTGCGCTGTGATGTGGCAGG---CGGCGCCAGCGTGAATTCATGCTGTGCGGCACTGT 477
 Db 1512 CTGGCAGCGGAGCGGAGAAAGTCAAGACAGACGCGAGTTCGAGGCGCTGAGGAGACTGC 1453
 Oy 478 ATCATCAAGATCTTCAAGTCTGATGGCTTGAAGGCGCTTACCAAGGCTTTCACAGCTCT 537

Db 1452 CTGCTGAAGATCAACCAAGTCCGAGCGCATCCGGGCGCTGTACCAAGGCTTCACTGTCTCC 1393
 Oy 538 GTCCAGACATCATTAATCTATAGACTGCTTCTGAGTCTATGATCTATGCAAGGGG 597
 Db 1392 GTCCAGGCGATCATCTATACCGCGCGGCTTCTGAGTCTATGATGCAAGGCGC 1333
 Oy 598 ATGCTGCTGACCCCAAGAACGTCACATTTTGTGAGCTGATGATGATGCGCAGAGTGT 657
 Db 1332 ATGCTGCTGACCCCAAGAACGTCACATGCTGATGATGATGATGCGCAGAGCTGT 1273
 Oy 658 ACGGAGTCCGAGCGCTGCTCTTCTTACACTTGTGACACTTGTGCTGATAGATGATG 717
 Db 1272 ACGGCGCTGCGCGCGCTGCTCTTCTTACACTTGTGACAGCGTGGCGCGCGCTGATGATG 1213
 Oy 718 CAGTCCGCGCGGAAAGGCGCGATTTATGATACCGGAGACTTGTGCTGAGGAGAG 777
 Db 1212 CAGTCCGCGCGGAAAGGAGCTGATCATCTATACAGCGGCGCGCTGCTGAGGAGAG 1153
 Oy 778 ATTGCAAAAGACAGAGAGCGGCTTCTTCAAGAGTCTGCTGCTGATGATGATGATG 837
 Db 1152 ATCTTCAAGATGAGAGGCGGCGGCTTCTTCAAGAGTCTGCTGCTGATGATGATGATG 1093
 Oy 838 GGCATGCGCGGCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 894
 Db 1092 GGCATGCGCGGCGCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1036
 RESULT 12
 AAD00520
 ID AAD00520 standard; cDNA; 897 BP.
 AC
 AC AAD00520:
 DT 29-AUG-2000 (first entry)
 XX
 DE Human adenine nucleotide translocator ANF2 cDNA.
 XX
 KW Human: adenine nucleotide translocator: ANF2; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurologic;
 KW antiParkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KW antiparkinsonian; cytoprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome; ss.
 KW
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..897
 FT /tag- a
 FT /product= "ANF2"
 XX
 PD WO200026370-A2.
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999: 99NO-US25883.
 XX
 PR 03-NOV-1998: 98US-0185904.
 PR 08-SEP-1999: 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR WPI: 2000-365619/31.
 DR P-PSDB: AAY71032.
 XX

PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease

PS Example 1: Page 165-166; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is a cDNA
 CC encoding adenine nucleotide translocator ANT2 from human brain.

XX Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other:

Query Match 61.9% Score 553; DB 21; Length 897;
 Best Local Similarity 76.8%; Pred. No. 9,6e-150;

Matches 689; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

OY 1 ATGGGTGATCAGCTTGGAGCTTCTTAAAGACCTTCGCGCGCGCGCTCCGCTCC 60
 DB 1 ATGACAGATGCCGCAATGCTTCTCCCAAGACCTTCGCGAGTGAGTGCGCCACCC 60
 OY 61 GTCTCCAGACCCGCGTCCGCTCCATCGAGAGGCTCAAACTCTCTGAGCTCCAGCAT 120
 DB 61 ATCTCCAGAGCGCGGTGAGCGCCCATCGAGCGGCTCAAGCTCTCTGAGCTCCAGCAT 120
 OY 121 GCCAGCAACAGATCAGCTCTGAGAGACAGTACAAAGGATCATTTGTCGTGAGA 180
 DB 121 GCCAGCAACAGATCAGCTCTGAGAGACAGTACAAAGGATCATTTGTCGTCTGCT 180
 OY 181 ATCCCTAAGGACGAGGCTCTCTCTCTGAGAGGCTTACCTGCGCAAGCTGATTCCT 240
 DB 181 ATCCCTAAGGACGAGGATCTCTCTCTGAGAGGCTTACCTGCGCAAGCTGATTCCT 240
 OY 241 TACTTCCCAAGGACGAGGATCTCTCTCTGAGAGGCTTACCTGCGCAAGCTGATTCCT 300
 DB 241 TACTTCCCAAGGACGAGGATCTCTCTCTGAGAGGCTTACCTGCGCAAGCTGATTCCT 300
 OY 301 GGGGCTGTGATGCGCATTAAGCAGTTCGCGCTACTTGTGCTGTAACCTGCGTCCGCT 360
 DB 301 GGGGCTGTGATGCGCATTAAGCAGTTCGCGCTACTTGTGCTGTAACCTGCGTCCGCT 360
 OY 361 GGGGCTGTGATGCGCATTAAGCAGTTCGCGCTACTTGTGCTGTAACCTGCGTCCGCT 420
 DB 361 GGGGCTGTGATGCGCATTAAGCAGTTCGCGCTACTTGTGCTGTAACCTGCGTCCGCT 420
 OY 421 TTGCGTGTGATGTCGCA---GGCGCGCCAGCGCTGAGTTCATGCTTGGCGCATCT 477
 DB 421 TTGCGTGTGATGTCGCA---GGCGCGCCAGCGCTGAGTTCATGCTTGGCGCATCT 477
 OY 481 CTGAGCAGCTGATGTGGTAACCTGAGCTGTAAGGCAATTCGAGGCGCTGGTACATGC 480
 DB 481 CTGAGCAGCTGATGTGGTAACCTGAGCTGTAAGGCAATTCGAGGCGCTGGTACATGC 480
 OY 478 ATCATCAAGATTTCAAGTCTGATGCGCTGAGGCGGCTCTACAGGCTTTCAGCTCTCT 537
 DB 478 ATCATCAAGATTTCAAGTCTGATGCGCTGAGGCGGCTCTACAGGCTTTCAGCTCTCT 537
 OY 538 GTCCAAGGATCATTAATGATGAGCTGCTGAGGCTGATGATATACCTCCAGGGG 597
 DB 538 GTCCAAGGATCATTAATGATGAGCTGCTGAGGCTGATGATATACCTCCAGGGG 597
 OY 541 ATGCTGCTGACCCCAAGAACGCTGACATTTTGTGAGCTGATGATGCGCAGAGTGTG 657
 DB 541 ATGCTGCTGACCCCAAGAACGCTGACATTTTGTGAGCTGATGATGCGCAGAGTGTG 657
 OY 601 ATGCTTCCGATGCCAAGAACACATCATGCTGATGATGATGATGATGATGATGATGAT 660
 DB 601 ATGCTTCCGATGCCAAGAACACATCATGCTGATGATGATGATGATGATGATGATGAT 660

OY 658 ACGCAGCTGCGAGGCTGCTCTACCCCTTTGACACTGTTCTGCTGAGATGATGTC 717
 DB 661 ACTGCTGTTGCCAGGGTTGACTTCTCTTACCTTACACCCCTTCCCGCCGATGATGTC 720
 OY 718 CAGTCCGCGCGGAGGCGGATATTATGATACAGGAGAGTGTGACTGCTGAGAG 777
 DB 721 CAGTCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 OY 778 ATTCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 837
 DB 781 ATTCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 OY 838 GCGATGCGGCTGCTTTTGTATGCTGTTGATGATGATGATGATGATGATGATGATGAT 894
 DB 841 GCGATGCGGCTGCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

RESULT 13
 ID AAS05902 standard; cDNA: 897 BP.
 AC AAS05902;
 XX 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) cDNA sequence.
 XX
 KW Human: adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes; mellitus; hyperproliferative disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT 1..897
 FT CDS /tag= a
 FT /product= "ANT-2"
 XX
 PN W0200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000MO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritgerl LG;
 PI Velicelebi G, Davis RE;
 PI
 DR MPI: 2001-291054/30.
 DR P-PSDB: AAU01199.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PS
 PS Disclosure: Fig 1: 186pp; English.
 XX
 CC The present sequence encodes for human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel

CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other:

Query Match 61.9%: Score 553; DB 22; Length 897;

Best Local Similarity 76.8%: Pred. No. 9.6e-150;

Matches 689; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

```

OY 1 ATGGGATATACGCTTGGAGCTTCTTAAAGACTTCTGCGCGGCGGCGCGCTGCC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 1 ATGACAGATGGCGATTGTCTTGGCCAGAGACTTCTGCGCAGGTGGAGTGGCGAGCC 60
OY 61 GTCTCAAGACCGCGTCCGCCCGCCAGAGGCTCAAACTGCTGTCGACAGTCCAGCAT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 61 ATCTCAAGACCGCGTACGCCCGCCAGAGGCTCAAACTGCTGTCGACAGTCCAGCAT 120
OY 121 CCCAGCAAGACGATCATGCTGAGAGACGATCAAAAGGATCATTTGCTGTGAGAGA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 121 GCCAGCAAGACGATCATGCTGAGAGACGATCAAAAGGATCATTTGCTGTGAGAGA 180
OY 181 ATCCCTAAGAGAGCGGCTTCTCTCTTCTGAGAGGCTTAACCTGCGCAACGATCCGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 181 ATCCCAAGAGAGCGGATTTCTCTCTTCTGAGAGGCTTAACCTGCGCAACGATCCGA 240
OY 241 TACTTCCCGACCCAGCTCTCAACTTGCCTTCAAGAGCAAGTACAGCACTTCTTTA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 241 TACTTCCCGACCCAGCTCTTAACTTGCCTTCAAGAGCAAGTACAGCACTTCTCTG 300
OY 301 GGGGCTGTGATCGGCATAGCACTTCTGCGGCTACTTCTGCTGAACCTGCGTCCGCT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 301 GGTGCTGTGACAGAGAACCCAGTTTGGCGCTACTTCTGCAAGCAATCTGGCATCGGCT 360
OY 361 GGGGCGCTGGGGGCGACCTCCCTTGTGCTTACCGCGGAGCTTGGTGAAGAGCAGG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 361 GGTGCGCGGAGGGGCGACATCCCTGTCTTGTGATCCCTCTTGATTTTGGCCGATCCGT 420
OY 421 TTGGCTGCTATGTGGCA--GGCGCGCGGAGCGTGCATTCGTCTGGCGCATCT 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 421 CTACAGAGCTGATGTGGGTAAGCTGAGACTGAAGAGAAATTCGAGCGCTGGTGACATGC 480
OY 478 ATCATCAAGATCTTCAAGCTTGATGGCTGAGGGGCTCTACAGAGGTTTCAAGCTCTCT 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 481 CTGGTTAAGATCTCAAAATCTGATGGGATTTAAGGGCTGTACCAAGGCTTTAAGCTGTCT 540
OY 538 GTCCAGGCAATCATTTATATATAGAGCTGCTACTTGGAGTCTATGATGACTGCCAAGGG 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 541 GTCCAGGCTATTTATCATCTTACCGAGCCGCTACTTCCGTATCTATGACATGCCAAGGGA 600
OY 598 ATGCTGCGCTGACCCCAAGAGCTGACATTTTGTGAGCTGGATGATTTGCCAGAGTGTG 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 601 ATGCTTCCGATCCCAAGACATCACTACATGCTCATGACTGGATGATGCCAGAGACTGTC 660
OY 658 ACGGCACTGCGAGGGGCTGCTCTTACCCCTTTGACACTGTTTCTGCTGAGAAATGATATG 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 661 ACTGCTGTGGCGGTTGACTTCTTATCCATTTGACACCTTTTGGCGCGGATGATGTATG 720
OY 718 CAGTCCGCGCGAAAGGGCGGATTTATGATACAGGGGAGAGTGTGATGCTGAGAGAG 777
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 721 CAGTCCAGGGCGCAAGAGACTGATCATCTATACAGAGCAGCGTTCATGCTGGGGAGAG 780
OY 778 ATTGCAAAAAGACGAGAGAGCAAGCGCTTCTTCAAAAGTGGCTGCTGAATGTGCTGAGA 837
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 781 ATTGCTGCTGATGAAGAGAGCAAAAGCTTTTTCAAAGGGTGCATGCTCAATGTCTCAGA 840
OY 838 GCGATGGGCGGCTTTTGTATGTGTGTGATGATGATCAAAAATATCTCTAA 894

```

Dd 841 GCGATGGGTGCTGCTTTTGTGCTTGTCTGATGATCAAAATCAAGAGTACACATTA 897

RESULT 14

AA516689

AA516689 standard; cDNA: 897 BP.

14-FEB-2002 (first entry)

DNA encoding human adenine nucleotide translocator 2 (ANT2).

Human; adenine nucleotide translocator; ANT; ss;

mitochondrial matrix protein.

Homo sapiens.

Location/Qualifiers

1..897

/*tag= a

/product= "Adenine nucleotide translocator 2 (ANT2)."

MO200185944-A2.

15-NOV-2001.

11-MAY-2001; 2001WO-US15416.

11-MAY-2000; 2000US-0569327.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo FR;

Ghosh SS, Moos WH, Pel Y, Carroll AK;

WP1: 2002-055598/07.

P-PSDB; MAU10379.

Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide

Example 1; Fig 1; 147pp: English.

The invention relates to a recombinant expression construct (1) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (1) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (1) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the coding sequence of human ANT2.

Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other:

Query Match 61.9%: Score 553; DB 24; Length 897;

Best Local Similarity 76.8%: Pred. No. 9.6e-150;

Matches 689; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

```

OY 1 ATGGGATATACGCTTGGAGCTTCTTAAAGACTTCTGCGCGGCGGCGCTGCC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 1 ATGACAGATGGCGATTGTCTTGGCCAGAGACTTCTGCGCAGGTGGAGTGGCGAGCC 60

```

```
OY 61 GTCTCAGACGGCGGTGCGCCCATCGAGAGGCTCAAACTGCTGTCAGAGT 120
DB 61 ATCTCCAAAGACGGCGGTGACGCCCATCGAGCGGCTCAAGCTGCTGTCAGAGT 120
OY 121 GCCAGCAAGACAGTCACTGCTGAGAGAGTACAAAGGATCATGATGCTGTGAGA 180
DB 121 GCCAGCAAGACAGTCACTGCTGAGAGAGTACAAAGGATCATGATGCTGTGAGA 180
OY 181 ATCCCTAAGAGCAGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 ATCCCTAAGAGCAGGAGATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
OY 241 TACTTCCCAACCCAGCTCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 TACTTCCCAACCCAGCTCTTAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
OY 301 GGGGCTGTGATGCGGATTAAGCAGTCTGAGGCTCTCTCTCTCTCTCTCTCTCT 360
DB 301 GGTGTGTGACAAAGAACCCAGTCTTGTGCGCTCTCTCTCTCTCTCTCTCTCT 360
OY 361 GGGGCGCGCTGGGGCACCCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 361 GGTGTGTGACAAAGAACCCAGTCTTGTGCGCTCTCTCTCTCTCTCTCTCTCT 420
OY 421 TTGGCTGTGATGCTGGCA---GGCGCGCGCGCTGAGTCTCTCTCTCTCTCTCT 477
DB 421 TTGGCTGTGATGCTGGCA---GGCGCGCGCGCTGAGTCTCTCTCTCTCTCTCT 477
OY 478 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGGCGCTCTCAAGGCTTCAAGCT 537
DB 478 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGGCGCTCTCAAGGCTTCAAGCT 537
OY 538 GTTCAAGGATCATATATATATGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 597
DB 538 GTTCAAGGATCATATATATATGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 597
OY 541 GTGCAAGGATATATATATATATGAGCTGCTCTCTCTCTCTCTCTCTCTCTCT 600
DB 541 GTGCAAGGATATATATATATATGAGCTGCTCTCTCTCTCTCTCTCTCTCTCT 600
OY 558 ATGCTGCTGACCCCAAGAGAGTGCATTTTGTGAGCTGATGCTGCTGCTGCTG 657
DB 558 ATGCTGCTGACCCCAAGAGAGTGCATTTTGTGAGCTGATGCTGCTGCTGCTG 657
OY 601 ATGCTTCCGGATCCCAAGAGAGTGCATTTTGTGAGCTGATGCTGCTGCTGCTG 660
DB 601 ATGCTTCCGGATCCCAAGAGAGTGCATTTTGTGAGCTGATGCTGCTGCTGCTG 660
OY 658 AGGCAAGTGCAGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 717
DB 658 AGGCAAGTGCAGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 717
OY 661 ACTGCTGTGCGGGTGTGACTTCTCTATTCATTTGACACCGTTCGGCGCGGAT 720
DB 661 ACTGCTGTGCGGGTGTGACTTCTCTATTCATTTGACACCGTTCGGCGCGGAT 720
OY 718 CAGTCCCGCGGCAAGGCGCGATTTATGTAACGGGAGAGTCTGCTGAGAG 777
DB 718 CAGTCCCGCGGCAAGGCGCGATTTATGTAACGGGAGAGTCTGCTGAGAG 777
OY 721 CAGTCAAGGCGCGCAAGAGTGCATTTTGTGAGGCGCTGCTGCTGCTGAG 780
DB 721 CAGTCAAGGCGCGCAAGAGTGCATTTTGTGAGGCGCTGCTGCTGCTGAG 780
OY 778 ATTGCAAAAGAGAGGAGGCGCTTCTCAAGGCGCTGCTGCTGCTGCTGAG 837
DB 778 ATTGCAAAAGAGAGGAGGCGCTTCTCAAGGCGCTGCTGCTGCTGCTGAG 837
OY 838 GCCATGCGCGCTGCTTCTATGCTGCTGATGATGATGATGATGATGATGATG 894
DB 838 GCCATGCGCGCTGCTTCTATGCTGCTGATGATGATGATGATGATGATGATG 894
OY 841 GGCATGGGTGCTTTTGTCTTCTTGTATGATGATGATGATGATGATGATG 897
DB 841 GGCATGGGTGCTTTTGTCTTCTTGTATGATGATGATGATGATGATGATG 897
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RESULT 15

AAS91243
ID AAS91243 standard; cDNA: 1156 BP.

AC AAS91243;

DE 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #27047.

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;

KM food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

XX

```
PN W0200175067-A2.  
XX 11-OCT-2001.  
PD 30-MAR-2001: 2001WO-US08631.  
XX 31-MAR-2000: 2000US-0540217.  
XX 23-AUG-2000: 2000US-0649167.  
XX (HSE-) HYSEQ INC.  
PA Drmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX P-PSDB: AB627056.  
DR New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
XX biodiversity.  
PS Claim 1: SEQ ID No 27047: 103pp: English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against it, detecting or  
XX quantitating a polypeptide in tissue, as molecular weight markers and as  
XX a food supplement. (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. AAS64197-AAS94564 represent novel human  
XX diagnostic coding sequences of the invention.  
XX Note: The sequence data for this patent did not appear in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published_pct_sequences.  
XX  
XX Sequence 1156 BP: 264 A: 286 C: 302 G: 303 T: 1 other:  
SQ  
Query Match 58.5%: Score 523.2: DB 23: Length 1156:  
Best Local Similarity 76.8%: Pred No. 4.5e-141:  
Matches 691: Conservative 0: Mismatches 203: Indels 6: Gaps 4:  
OY 1 ATGGGTGATCAAGCTTGGAGCTTCTTAAGAGCTTCTGCGCGGCGGTGCGCGCTCC 60  
DB 53 ATGACAGATGCGCGGTGCTGCTCTCCCAAGAGCTTCTGCGAGGTGAGGTGCGCGCACCC 112  
OY 61 GTTCTCAGAGCGCGGTGCGCGCGCATGAGAGGTCTCAAACTGCTGCTGCTGAGCAT 120  
DB 113 ATCTCCAAAGAGCGCGGTGAGCGCGCTTCAAGGCGCTGCTGCTGCTGCTGAGAT 172  
OY 121 GCCAGCAAGACAGTCACTGCTGAGAGAGTACAAAGGATCATGATGCTGTGAGA 180  
DB 173 GCCAGCAAGACAGTCACTGCTGAGAGAGTACAAAGGATCATGATGCTGTGAGA 232  
OY 181 ATCCCTAAGAGCAGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
DB 233 ATCCCAAGAGCAGGAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 292  
OY 241 TACTTCCCAACCCAGCTCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
DB 293 TACTTCCCAACCCAGCTCTTAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 352  
OY 301 GGGGCTGTGATGCGGATTAAGCAGTCTGAGGCTCTCTCTCTCTCTCTCTCTCT 360  
DB 301 GGTGTGTGACAAAGAACCCAGTCTTGTGCGCTCTCTCTCTCTCTCTCTCTCT 360
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Db 353 GGTGCTGTGACAGAGAACCCAGTTTGGCCCTACTTTGACAGGAATCTGGCATCGGCT 412
 QY 361 GGGGGCCGCTGGGGCCACCTCCCTTTGCTTGTCTACCCCTGGACTTTGCTAGACAGG 420
 Db 413 GGTGCCGACAGGGCCACATCCCTGTGTGTTGTTACCCCTTGTGATTTTGGCCGTACCCGT 472
 QY 421 TTGGCTGCTGATGTGGCA---GGCGGCCACAGCGTAGTTCATGCTGGGGGACTGT 477
 Db 473 CTAGCAGCTGATGTGGGTAAAGCTGAGCTGAAAGGAAATCCGAGGCCCTCGGTGACTGC 532
 QY 478 ATCATCAGATCTTCAAGTGTGATGGCTGAGGGGGCTCTACAGGGTTTCAACGTCTCT 537
 Db 533 CTGGTTAAGATCTACAAATCTGTATGGGATTTAAGGCCCTGACCAAGGCTTTAAGCTGTCT 592
 QY 538 GTTCAAGGCATCATTTATATAGAGCTGCTTACTTGGAGTCTATGATACGCCAAGGGG 597
 Db 593 GTGCAGGGTATTATCATCTACCGAGCGGCTTACTTGGTATCTATGACACTGCMAAGGGA 652
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 Db 653 ATGCTTCCGGATCCCAAGAACACTCAGATGTCATCAGCTGGATGATGCCACAGACTGTC 712
 QY 658 ACGGCACTCCAGAGGCTGCTGTCTTACCCCTTTGACACTGTTGCTAGTAATGATGATG 717
 Db 713 ACTGCTGTGGCGGTTGACTTCTTATCCATTGACACGTGTGCGCGGCATGATGATG 772
 QY 718 CAGTCCGCGGCAAGAGGGCCGATTTATGTCACGGGACAGTGTGCTGGAGGAAG 777
 Db 773 CAGTCAGGGCGCAAGAGACTGACATCATGTACACAGGCACGCTTACTGTGGCGGAAG 832
 QY 778 ATTGC-AAAAGAGAGAGAGCCCAAGGCTTCTCAAAAGTGCCCTGGTCCAATG-TGCTGA 835
 Db 833 ATTGCTCCGTGATGAGAGAGCAAGCTTTTTCAGGGGTGATGATGCTCAATGTTCTCA 892
 QY 836 GAGGCATGGCGGCTGCTTTTGTATGTGTTGT-ATGATGAGATCAAAAAATATGCTTAA 894
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Search completed: June 22, 2003, 03:22:31
 Job time : 196 secs

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 01:58:09 ; Search time 46 Seconds
(without alignments)
5960.196 Million cell updates/sec

Title: US-09-393-441-1

Perfect score: 894
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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3: /cgnt2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgnt2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgnt2_6/prodata/1/ina/PCrus_COMB.seq.*
6: /cgnt2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	746.6	83.5	1259	3 US-08-961-871-11	Sequence 11, Appl
2	745	83.3	1177	3 US-08-961-871-9	Sequence 9, Appl
3	46.6	5.2	1255	1 US-08-518-878B-38	Sequence 38, Appl
4	46.6	5.2	1255	1 US-08-294-522B-38	Sequence 38, Appl
5	46.6	5.2	1255	2 US-08-470-868A-38	Sequence 38, Appl
6	46.6	5.2	1596	2 US-08-807-861A-38	Sequence 38, Appl
7	46.6	5.2	1596	3 US-09-210-681-38	Sequence 38, Appl
8	46.6	5.2	1596	3 US-08-946-719A-38	Sequence 38, Appl
9	42	4.7	1192	4 US-09-142-565-1	Sequence 1, Appl
10	39.2	4.4	810	1 US-08-642-255-60	Sequence 60, Appl
11	37.8	4.2	1643	2 US-08-933-750C-68	Sequence 68, Appl
12	37.8	4.2	1643	3 US-09-234-613-68	Sequence 68, Appl
13	37.4	4.2	997	3 US-09-188-930-23	Sequence 23, Appl
14	37.4	4.2	1816	3 US-09-188-930-262	Sequence 262, App
15	37	4.1	1777	2 US-08-937-466-5	Sequence 5, Appl
16	37	4.1	1777	2 US-09-172-528-5	Sequence 5, Appl
17	37	4.1	1777	3 US-09-318-199-5	Sequence 5, Appl
18	37	4.1	1777	4 US-09-503-579-5	Sequence 5, Appl
19	37	4.1	1949	2 US-08-937-466-3	Sequence 3, Appl
20	37	4.1	1949	2 US-09-172-528-3	Sequence 3, Appl
21	37	4.1	1949	3 US-09-318-199-3	Sequence 3, Appl
22	37	4.1	1949	4 US-09-503-579-3	Sequence 3, Appl
23	37	4.1	2782	2 US-08-937-466-1	Sequence 1, Appl
24	37	4.1	2782	2 US-09-172-528-1	Sequence 1, Appl
25	37	4.1	2782	2 US-09-318-199-1	Sequence 1, Appl
26	37	4.1	2782	4 US-09-503-579-1	Sequence 1, Appl
27	35.4	4.0	216	1 US-07-972-032-46	Sequence 46, Appl

C	28	34.4	3.8	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C	29	34.4	3.8	4411529	4	US-09-103-840A-1	Sequence 1, Appl
C	30	33.8	3.8	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C	31	33.8	3.8	4411529	4	US-09-103-840A-1	Sequence 1, Appl
C	32	33.6	3.8	1594	2	US-08-933-750C-61	Sequence 61, Appl
C	33	33.6	3.8	1594	3	US-09-234-613-61	Sequence 61, Appl
C	34	33.4	3.7	1435	4	US-09-153-804-4	Sequence 4, Appl
C	35	33.4	3.7	68750	3	US-09-335-409-1	Sequence 1, Appl
C	36	33.4	3.7	68750	4	US-09-568-102-1	Sequence 1, Appl
C	37	33.4	3.7	68750	4	US-09-567-969-1	Sequence 1, Appl
C	38	33.4	3.7	68750	4	US-09-568-480-1	Sequence 1, Appl
C	39	33.4	3.7	68750	4	US-09-568-486-1	Sequence 1, Appl
C	40	33.4	3.7	68750	4	US-09-568-472-1	Sequence 1, Appl
C	41	33.4	3.7	68750	4	US-09-567-899-1	Sequence 1, Appl
C	42	33.4	3.7	71969	4	US-09-443-501A-2	Sequence 2, Appl
C	43	33.2	3.7	4843	3	US-08-986-485-1	Sequence 1, Appl
C	44	33	3.7	1386	3	US-08-247-475-16	Sequence 16, Appl
C	45	33	3.7	1386	1	US-08-479-650-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-961-871-11
Sequence 11, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 190..1086
US-08-961-871-11

Query Match 83.5% Score 746.6 DB 3: Length 1259;
 Best Local Similarity 90.3% Pred. No. 5.2e+205;
 Matches 810; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

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Oy 1 ATGGGTGATACAGCTTGGAGCTTCTTAAGAGACTTCCTGGCGGGGCGGTGCGCCCTCC 60
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Db 190 ATGGGGGATCAGCGCTTTAGCTTCTTAAGAGACTTCCTGGCGAGGTGGCATGCGCCGCC 249

Oy 61 GTCCTCAAGACCGCGGCTGCGCCCATCGAGAGGGTCAAACTGCTGCTCAGCTCCAGCAT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 GTCCTCAAGACCGCGGCTGCGCCCATCGAGAGGGTCAAACTGCTGCTCAGCTCCAGCAT 309

Oy 121 GCCAGCAACAGATCAGCTGCTGAGAGAGTACAAAGGAGTATGTTGTGTGTGAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 310 GCCAGCAACAGATCAGCTGCTGAGAGAGTACAAAGGAGTATGTTGTGTGTGAGA 369

Oy 181 ATCCCTAGAGAGAGCGCTTCTCTCTCTGAGAGGGTAACTGCGCCAGGTATCCGT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 370 ATCCCAAGAGAGAGCGCTTCTCTCTCTGAGAGGGTAACTGCGCCAGGTATCCGT 429

Oy 241 TACTTCCCAACCAAGCTCTCAACTTCCCTTCAAGAGAGTACAGACAGCTTCTTCTTA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 430 TACTTCCCACTCAAGCCCTGACACTTCCCTTCAAGAGAGTACAGACAGATCTTCTCTG 489

Oy 301 GGGGGTGTGATCGGCATTAAGCAGTCTGCGGCTACTTGTCTGCTGATACCTGCGCT 360
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Db 490 GGAGCGGTGATCGGCATTAAGCAGTCTGCGGCTACTTGTCTGCTGATACCTGCGCT 549

Oy 361 GGGGCGCTGGGCGCCACTCCCTCTTGTCTACTCCGCTGAGACTTGTCTAGAGACAG 420
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Db 550 GGGGCGCTGGGCGCCACTCCCTCTTGTCTACTCCGCTGAGACTTGTCTAGAGACAG 609

Oy 421 TTGCTGCTGATGTGGCAGGCG---CGCCAGCGTGAATTCATGCTTGGCGCACTGT 477-
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Db 610 CTGGCTGCGAGCTGGCGAGGAGATCTTCCAGCAGAGTAATCAATGGCGTGGCGCACTGT 669

Oy 478 ATCATCAGATCTTCAAGTCTGATGCGCTGAGAGGGGCTCTACAGAGGTTTCAACGTCTCT 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 670 CTCACCAAGATCTTCAAGTCTGATGCGCTGAGAGGGGCTCTACAGAGGTTTCAAGTCTCT 729

Oy 538 GTCCAAGCATCATATCTATATAGAGCTGCTACTTCCGAGTCTATGACTGCCAAGGGG 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 730 GTCCAAGCATCATATCTATATAGAGCTGCTACTTCCGAGTCTATGACTGCCAAGGGG 789

Oy 598 ATGCTGCTGACCCCAAGACGTGCACATTTTGTGAGCTGGATGATTTGCCAGAGTGTG 657
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Db 790 ATGCTGCTGACCCCAAGACGTGCACATTTTGTGAGCTGGATGATTTGCCAGAGTGTG 849

Oy 658 ACGGCACTGCGAGGGGCTGCTCTCAACCCCTTTGACACTGTTTCTGCTAGATATGATG 717
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Db 850 ACAAGGCTGCGAGGGGCTGCTCTCAACCCCTTTGACACTGTTTCTGCTAGATATGATG 909

Oy 718 CAGTCCGCGCGGAAAGGGGCGATATATATGACAGGGGACAGTGTGCTGAGAGAG 777
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Db 910 CAGTCCGCGCGGAAAGGGGCGATATATATGACAGGGGACAGTGTGCTGAGAGAG 969

Oy 778 ATTGCAAAAGACGAAGAGCCAGAGCCCTTTTCAAGGTGCTGCTCAATGTGTGAGA 837
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Db 970 ATTGCAAAAGATGAAGAGCCAGAGCCCTTTTCAAGGTGCTGCTCAATGTGTGAGA 1029

Oy 838 GGCATGGGCGGCTTTGTATGTGTTGTATGATGATGATCAAAAAATATGTCTAA 894
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Db 1030 GGCATGGGCGGCTTTGTATGTGTTGTATGATGATGATCAAAAAATATGTCTAA 1086
  
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RESULT 2
 US-08-961-871-9
 ; Sequence 9, Application US/08961871
 ; Patent No. 6013858
 ; GENERAL INFORMATION:
 ; APPLICANT: Wallace, Douglas C.
 ; APPLICANT: Graham, Brett H.
 ; APPLICANT: Macgregor, Grant R.

TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
 Nucleotide Translocator Protein and Methods
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Minner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle, Suite 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/961,871
 FILING DATE: 31-OCT-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/030,017
 FILING DATE: 01-NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferber, Donna M.
 REGISTRATION NUMBER: 33,878
 REFERENCE/DOCKET NUMBER: 78-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1177 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 94...990
 US-08-961-871-9

Query Match 83.3% Score 745; DB 3: Length 1177;
 Best Local Similarity 90.2% Pred. No. 1.4e+204;
 Matches 809; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

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Oy 1 ATGGGTGATACAGCTTGGAGCTTCTTAAGAGACTTCCTGGCGGGGCGGTGCGCCCTCC 60
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Db 94 ATGGGGGATCAGCGCTTTGAGCTTCTTAAGAGACTTCCTGGCGAGGTGGCATGCGCGGCC 153

Oy 61 GTCCTCAAGACCGCGGCTGCGCCCATCGAGAGGGTCAAACTGCTGCTGAGAGTCCAGCAT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154 GTCCTCAAGACCGCGGCTGCGCCCATCGAGAGGGTCAAACTGCTGCTGAGAGTCCAGCAT 213

Oy 121 GCCAGCAACAGATCAGTGTGAGAGCAGTACAAAGGAGTATGATTGTGTGTGAGA 180
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Db 214 GCCAGCAACAGATCAGTGTGAGAGCAGTACAAAGGAGTATGATTGTGTGTGAGA 273

Oy 181 ATCCCTAGAGAGAGCGCTTCTCTCTCTGAGAGGGGTAACCTGCGCCAGCATATCCGT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 ATCCCAAGAGAGAGCGCTTCTCTCTCTGAGAGGGGTAACCTGCGCCAGCATATCCGT 333

Oy 241 TACTTCCCAACCAAGCTCTCAACTTCCCTTCAAGAGAGTACAGACAGCTTCTTCTTA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 TACTTCCCACTCAAGCCCTGACACTTCCCTTCAAGAGAGTACAGACAGATCTTCTCTG 393

Oy 301 GGGGGTGTGATCGGCATTAAGCAGTCTGCGGCTACTTGTCTGCTGATACCTGCGCT 360
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Db 394 GGAGCGTGTGATCGACATTAAGCAGTCTGCGGCTACTTGTCTGCTGATACCTGCGCT 453

Oy 361 GGGGCGCTGGGCGCCACTCCCTTGTCTACTACCCGCTGGAGCTTGTCTAGAGACAGG 420
  
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: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-518-878B-38
Query Match 5.2%; Score 46.6; DB 1; Length 1255;
Best Local Similarity 44.2%; Pred. No. 0.00067;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

DB 454 GGGGAGCTGGGGGACCTCTCTGCTGTACCCCGAGCTTGGTAGGACCG 513
OY 421 TTGCTGCTGATGTGGGACGCG---CGCCAGCGTGAAGTTCATGTCTGGGCACTGT 477
DB 514 CTGGCTGGGACGAGGAGGATCTTCCAGGAGAAATTCATGTGGGCTGGGCACTGT 573
OY 478 ATCATCAAGATCTTCAAGTCTGATGGCCCTGAGGGGCTCTACAGGGTTTCAAGCTCTCT 537
DB 574 CTCACCAAGATCTTCAAGTCTGAGGGGCTCTACAGGGTTTCAAGTCTCTCT 633
OY 538 GTCCAGGATCATTTATATATAGAGCTGCTACTTTCGAGTCTATGATGAGTCCCAAGGG 597
DB 634 GTCCAGGATCATTTATATAGAGCTGCTACTTTCGAGTCTATGATGAGTCCCAAGGG 693
OY 598 ATGCTGCTGACCCCAAGAGACGTCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657
DB 694 ATGCTGCTGACCCCAAGAGATGTGACATTTATGCGAGCTGATGATTTGCCAGAGTGTG 753
OY 658 ACAGGATGTCAGAGGCTGCTCTACCCCTTTGACACTGTTCTGATGATGATGATG 717
DB 754 ACAGGATGTCAGAGGCTGCTCTATCTTATCTGTTGACACTGTTCTGATGATGATG 813
OY 718 CAGTCCGCGCGAAGGGGCGGATATTTATGACAGGGGACAGTTGACTGCTGGAGGAG 777
DB 814 CAGTCCGCGCGAAGGGGCGGATATTTATGACAGGGGACAGTTGACTGCTGGAGGAG 873
OY 778 ATTCGAAAGAGAGAGGAGCCAGCTTCTTCAAGAGTGGCTGCTCAATGCTGAGAG 837
DB 874 ATTCGAAAGAGAGAGGAGCCAGCTTCTTCAAGAGTGGCTGCTCAATGCTGAGAG 933
OY 838 GCGATGGCGGCTGCTTTTGTATGTGTTGATGATGATGATGATGATGATGATG 894
DB 934 GCGATGGCGGCTGCTTTTGTATGTGTTGATGATGATGATGATGATGATGATG 990

RESULT 3
US-08-518-878B-38
: Sequence 38, Application US/08518878B
: Patent No. 5702902
: GENERAL INFORMATION:
: APPLICANT: Tartaglia, Louis A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/518,878B
: FILING DATE: 23-AUG-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7853-036
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEFAX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 38:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1255 base pairs
: TYPE: nucleic acid

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: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-518-878B-38
Query Match 5.2%; Score 46.6; DB 1; Length 1255;
Best Local Similarity 44.2%; Pred. No. 0.00067;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

DB 455 AGTTCATGCTCTGGGCGACGTGATCATCAAGATCTTCAAGTGTGATGGCTGAGGGGGC 514
DB 143 AGTACCGGGGTGTGTGGGACACATTTCTGACATGTGCTGACTGAGGGGCCCGAAGCC 202
OY 515 TCTACCAAGGTTTCAAGCTCTCTGTCGCAAGCATCATATATATGAGCTGCTACTTTCG 574
DB 203 TCTACCAAGGCTGTGTTTCCGCGCTGCGGCGCAAGATGCTTTCCTGCTGCTGCTGCTG 262
OY 575 GAGTCTATGATGATGCTCCAGAGGAGTGTGCTGACCCCAAGACGTCGACATTTTCTGGA 634
DB 263 GCCTGTATGATTTCTGTCAACAGATTCTACACCAAGGGCTGTGAGCATGCCAGCATTTGGGA 322
OY 635 GCTGGATGATTTCCAGAGTGTGACGCGAGTGTGCGAGGGCTGCTGCTACCCCTTTGACA 694
DB 323 GCGGCTCTCTAGCAGGCGACACACAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 382
OY 695 CTGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 754
DB 383 ATGTGCTAAGAGTCCGATTTCCAGCTCAGGCGCGGCTGCGAGTGTGCGAGATGACAAA 442
OY 755 GCACAGTGTGATGCTGAGAGATTTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
DB 443 GCACCGTCAATGCCCTACAGAGACATTTGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 502
OY 815 GTGCTGTGCTCAAGTGTGAGAGAGCATGAGGCGGCTGTTTGTATGTGTTGATGATG 874
DB 503 GACCTCTCCCAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 562
OY 875 AGATCAAAAATATGTC 891
DB 563 ACCTCATCAAGATGCC 579

RESULT 4
US-08-294-522B-38
: Sequence 38, Application US/08294522B
: Patent No. 5741666
: GENERAL INFORMATION:
: APPLICANT: Tartaglia, Louis A.
: TITLE OF INVENTION: Compositions and Methods for the
: Treatment of Body Weight Disorders, Including Obesity
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/294,522B
: FILING DATE: 23-AUG-1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7853-015
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: INFORMATION FOR SEQ ID NO: 38:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-522B-38

Query Match 5.2% Score 46.6; DB 1; Length 1255;
Best Local Similarity 44.2% Pred. No. 0.00067;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

455 ACTTCATGCTGCGGCGACATGATCATCATCTTCAAGTCTGATGCGCTGAGGGGCG 514
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
143 AGTACCGCGGTGTGATGGCGACCATTTCTACCATGTGGCTACTGAGGCCCCCAAGCC 202
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
515 TCTACCAAGGTTTCAACGCTCTCTGTCGAAGGCATCTATATAGAGCTGCGCTACTTGC 574
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
203 TCTACAAATGGCGCTGGTGGCGCGCTGACGCGCAATGAGCTTTGGCTCTGTCGCGATCG 262
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
575 GAGCTATGATACTGCGCAAGGGGATGCTGCTGACGCCCAAGAACGTCACATTTTGTGA 634
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
263 GCGCTATGATTTCTGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCGCACATTTGGGA 322
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
635 GCTGATGATGTCGCCAGACTGTGACGGCGAGTCGCGAGGCTGCTGTCTACCCCTTTGACA 694
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
323 GCGGCTCTCTAGCAGGACGACACACAGTGCTGCTGTGCTGTGCGCCACGCCACGG 382
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
695 CTGTTGCTGTAAGATGATGATGCAAGTCGCGCGGAAAGGGCCGATATTATATGACACGG 754
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
383 ATGTGTAAGGTCCGATTCGAAGCTCAAGCGCCGCGGCTGAGAGTGTCGAGATACCAAA 442
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
755 GCACAGTTGACTGCTGAGAGAGATTGCAAAAGACGAAGACCAAGGCTTCTTCAAG 814
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
443 GCACCGTCAATGCTCTACAGACCATTTGCCGAGAGAGAGGTTCCGGGCGCTGTGGAAG 502
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815 GTGCGTGTGCAATGTGCTGAGAGGACATGGCGGCTGTTGTATTTGTTGTTATGATG 874
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
503 GGACCTCTCCCAATGTGCTGTAATGCCATTGTCACTGTGCTGAGCTGTGACCTATG 562
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
875 AGATCAAAAATATATGTC 891
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
563 ACCTCATCAAGATGCC 579
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

RESULT 5
US-08-470-868A-38
Sequence 38, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-38

Query Match 5.2% Score 46.6; DB 2; Length 1255;
Best Local Similarity 44.2% Pred. No. 0.00067;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

455 ACTTCATGCTGCGGCGACATGATCATCATCTTCAAGTCTGATGCGCTGAGGGGCG 514
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
143 AGTACCGCGGTGTGATGGCGACCATTTCTACCATGTGGCTACTGAGGCCCCCAAGCC 202
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
515 TCTACCAAGGTTTCAACGCTCTCTGTCGAAGGCATCTATATAGAGCTGCGCTACTTGC 574
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
203 TCTACAAATGGCGCTGGTGGCGCGCTGACGCGCAATGAGCTTTGGCTCTGTCGCGATCG 262
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
575 GAGCTATGATACTGCGCAAGGGGATGCTGCTGACGCCCAAGAACGTCACATTTTGTGA 634
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
263 GCGCTATGATTTCTGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCGCACATTTGGGA 322
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
635 GCTGATGATGTCGCCAGACTGTGACGGCGAGTCGCGAGGCTGCTGTCTACCCCTTTGACA 694
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
323 GCGGCTCTCTAGCAGGACGACACACAGTGCTGCTGTGCTGTGCGCCACGCCACGG 382
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
695 CTGTTGCTGTAAGATGATGATGCAAGTCGCGCGGAAAGGGCCGATATTATATGACACGG 754
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
383 ATGTGTAAGGTCCGATTCGAAGCTCAAGCGCCGCGGCTGAGAGTGTCGAGATACCAAA 442
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
755 GCACAGTTGACTGCTGAGAGAGATTGCAAAAGACGAAGACCAAGGCTTCTTCAAG 814
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
443 GCACCGTCAATGCTCTACAGACCATTTGCCGAGAGAGAGGTTCCGGGCGCTGTGGAAG 502
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
815 GTGCGTGTGCAATGTGCTGAGAGGACATGGCGGCTGTTGTATTTGTTGTTATGATG 874
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
503 GGACCTCTCCCAATGTGCTGTAATGCCATTGTCACTGTGCTGAGCTGTGACCTATG 562
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
875 AGATCAAAAATATATGTC 891
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
563 ACCTCATCAAGATGCC 579
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

RESULT 6
US-08-807-861A-38
Sequence 38, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997


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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-807-861A-38

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Query Match      5.2%: Score 46.6; DB 2; Length 1596;
Best Local Similarity 44.2%; Pred. No. 0.00074;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

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OY 455 AGTTCATGCTGCTGGGAGCTATCATCAAGATCTTCAAGTGTGATGCTGAGGGGC 514
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DB 485 AGTACCGCGGTGTATGCGACACATCTGACATGTCGTCGTCGAGGGCCCGAAGCC 544
OY 515 TCTACAGGGTTTCAAGCTCTCTGTCCAGGCATCATTTATATAGAGCTGCTACTTCG 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 545 TCTACATGCGCTGCTGCGCGCTGCGACCGCCCAATGAGCTTTCCTGTCGCGATCG 604
OY 575 GAGCTATGATGATGCGCAAGGGGATGCTGCTGACCCCAAGACCTGACATTTTGTGA 634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 605 GCGTGTATGATGCTGTCAACAGTTTACACCAAGGGCTCTGACATGCGCATTTGGGA 664
OY 635 GGTGATGATGATGCGCAAGGGGATGCTGCTGACCGGCTGCTGCTGCTGCTGCTGCTG 694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 665 GCGCGCTCTGACGAGGACGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724
OY 695 CTGTTCTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 725 ATGTGTAAAGGTCGATTCACAGCTCAGCGCCGCGGTGAGGTGCGAGATACCAAA 784
OY 755 GGACAGTTGATGCTGAGAGGAGATTTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 814
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 785 GCACCGTCAATGCTTACAGAGACATTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
OY 815 GTGCGTGTGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 845 GGACCTCTCCCAATGTCGTCTGTAATGCAATGTCATGCTGCTGAGCTGTGACCTATG 904
OY 875 AGATCAAAAATATATGTC 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 905 ACCTCATCAAGATGCG 921
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 7
US-09-210-681-38
Sequence 38, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP

```

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-210-681-38

```

```

Query Match      5.2%: Score 46.6; DB 3; Length 1596;
Best Local Similarity 44.2%; Pred. No. 0.00074;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

```

```

OY 455 AGTTCATGCTGCTGGGAGCTATCATCAAGATCTTCAAGTGTGATGCTGAGGGGC 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 485 AGTACCGCGGTGTATGCGACACATCTGACATGTCGTCGTCGAGGGCCCGAAGCC 544
OY 515 TCTACAGGGTTTCAAGCTCTCTGTCCAGGCATCATTTATATAGAGCTGCTACTTCG 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 545 TCTACATGCGCTGCTGCGCGCTGCGACCGCCCAATGAGCTTTCCTGTCGCGATCG 604
OY 575 GAGCTATGATGATGCGCAAGGGGATGCTGCTGACCCCAAGAGAGAGAGAGAGAGAGAG 634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 605 GCGTGTATGATGCTGTCAACAGTTTACACCAAGGGCTCTGACATGCGCATTTGGGA 664
OY 635 GGTGATGATGATGCGCAAGGGGATGCTGCTGACCGGCTGCTGCTGCTGCTGCTGCTG 694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 665 GCGCGCTCTGACGAGGACGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724
OY 695 CTGTTCTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 725 ATGTGTAAAGGTCGATTCACAGCTCAGCGCCGCGGTGAGGTGCGAGATACCAAA 784
OY 755 GGACAGTTGATGCTGAGAGGAGATTTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 814
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 785 GCACCGTCAATGCTTACAGAGACATTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
OY 815 GTGCGTGTGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 845 GGACCTCTCCCAATGTCGTCTGTAATGCAATGTCATGCTGCTGAGCTGTGACCTATG 904
OY 875 AGATCAAAAATATATGTC 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Berttram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/B1R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
US-08-642-255-60

Query Match 4.4%; Score 39.2; DB 1; Length 810;
Best Local Similarity 50.5%; Pred. No. 0.074;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 23 TCCTAAGGACTTCCTGGCGGGGGCGGTGCGCCCTCCGCTCCAGACCGCGGTGCCC 82
DB 597 TGCCTCCGGGACCTCGACGCCACCGGCTACCGCTGCGCGGACCGCGGTGCGCC 656
QY 83 CCATCGAGAGGCTCAACTGCTGCTGAGATGCCAGATGCCAAGAGATGAGTGC 142
DB 657 TGGCCCAAGCGGCTCCGCTGATCTAGAGTGACCCAGACCGCTGCTGCGCATGCCC 716
QY 143 AGAAGCAGTACAAGGAGATCATTTGATGTGTGAGAAATCCCTAAGAGACGAGCTTC 202
DB 717 ACCAGACCGAAGAGAGCTTCACGCTCCGCGAGGTCCGAAACACAGGGGTACCGGCTC 776
QY 203 TCTCTTTC 210
DB 777 TGGCTTTC 784

RESULT 11
US-08-933-750C-68
Sequence 68, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Cortley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNOCAT01
CLONE: 724157
US-08-933-750C-68

Query Match 4.2%; Score 37.8; DB 2; Length 1643;
Best Local Similarity 48.4%; Pred. No. 0.25;
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 151 TACAAGGATCATTTATTTGTGTGTGAGAAATCCCTAAGAGACGAGGCTTCTCTCTTC 210
DB 490 TTCACCTGGGACCTGATGCTTCGTGAAGATGTGAGGACGACGACGACGACGAC 549
QY 211 TGGAGGGTAACTGGCCCAACGATCCGTACTTCCCAACCACTCTCACTTCCGC 270
DB 550 TGGAGGGGCTTCCCGCCACCTGATGATGACTGTGCACTACCCGATCTACTTCACT 609
QY 271 TTCAAGCAAGTACAAGCAAGCTCTTCTTAAGGGGTGTGATGCGCATAGCAGTTCTG 330
DB 610 CCTATGACCAACTGAAGGCTTCTGTGTGTGAGACCTGACCTCTGACCTCTACGCA 669
QY 331 CGCTACTTGTGCTGTAACCTGCGGCTCGGCGGCGCG 367
DB 670 CCCATGTGTGCTGCGCGCTGCGCGCTTGGGCGCG 706

RESULT 12
US-09-234-613-68
Sequence 68, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Cortley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive

```

1 CITY: Palo Alto
2 STATE: CA
3 COUNTRY: USA
4 ZIP: 94304
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Diskette
8 COMPUTER: IBM Compatible
9 OPERATING SYSTEM: DOS
10 SOFTWARE: FASTSEQ for Windows Version 2.0
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/234.613
14 FILING DATE:
15 CLASSIFICATION:
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US/08/933.750
18 FILING DATE: September 23, 1997
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Billings, Lucy J.
21 REGISTRATION NUMBER: 36,749
22 REFERENCE/DOCKET NUMBER: PF-0356 US
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 415-855-0555
25 TELEFAX: 415-845-4166
26 TELEX:
27
28 INFORMATION FOR SEQ ID NO: 68:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 1643 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 IMMEDIATE SOURCE:
35 LIBRARY: SYNCOAT01
36 CLONE: 724157
37
38 US-09-234-613-68
39
40 Query Match 4.2%; Score 37.8; DB 3; Length 1643;
41 Best Local Similarity 48.4%; Pred. No. 0.25; Indels 0
42 Matches 105; Conservative 0; Mismatches 112; Gaps 0
43
44 QY 151 TACAAGGAGCATATTGATGTGTGGAGAAATCCCTAAGACAGAGCGCTTCCTTCCTTC 210
45 111 111 111 111 111 111 111 111 111 111 111 111 111 111
46 DB 490 TTCACGTGGCACCATGATGATGCCCTGTGTGAAGATCGTAGAGCAGACGACGACCCCTC 549
47
48 QY 211 TCGAGGGGTAACTGGGCCAACGTGATCCGTTACTTCCCCACCACCAAGCTCTCAACTTCGCC 270
49 111 111 111 111 111 111 111 111 111 111 111 111 111 111
50 DB 550 TGGAGCGGCCCTCCCGCCACCCCTGTGATGACTGTGCCAGCTACCGCCATCTACTTCACT 609
51
52 QY 271 TTCAAGAGCAGATCAAGACACTCTCTCTTAAAGGGGTGTGGATTCGCATTAAGCAGTTTCG 330
53 111 111 111 111 111 111 111 111 111 111 111 111 111 111
54 DB 610 GCCATGACCACTGAAGGCCCTTCTCTGTGTGAGAGCCCTGACCTCTGACCTCTTACGCA 669
55
56 QY 331 CGTACTTTCCTGCTGAACCTGGCGTCCGCTGGGGCGC 367
57 111 111 111 111 111 111 111 111 111 111 111 111 111 111
58 DB 670 CCCATGGTGGCTGGCGCCGCTGGCCGCTTGGGGCACC 706
59
60 RESULT 13
61 US-09-188-930-23
62 Sequence 23, Application US/09188930A
63 Patent No. 6150502
64
65 GENERAL INFORMATION:
66
67 APPLICANT: Watson, James D.
68 APPLICANT: Strachan, Lorna
69 APPLICANT: Sleeman, Matthew
70 APPLICANT: Onrust, Rene
71 APPLICANT: Murlison, James Greg
72
73 TITLE OF INVENTION: Compositions Isolated From Skin Cells
74 TITLE OF INVENTION: and Methods for Their Use
75
76 FILE REFERENCE: 11000.1011c1
77 CURRENT APPLICATION NUMBER: US/09/188.930A
78 CURRENT FILING DATE: 1998-11-09
79 NUMBER OF SEQ ID NOS: 348
80
81 SOFTWARE: FASTSEQ for Windows Version 3.0

```

```

: SEQ ID NO 23
: LENGTH: 997
: TYPE: DNA
: ORGANISM: mouse
US-09-188-930-23

Query Match
Best Local Similarity 55.9%; Score 37.4; DB 3; Length 997;
Matches 71: Conservative 0; Mismatches 56; Indels 0; Gaps 0;

OY 10 CACGCTTGAGACTTCTAAAGAGACTTCGTGCGCGGGCGGTGCCGCTGCCGTCTCAAG 69
Db 605 CAGACGGGAGATGCTGTGAGGACGACCTGCTGCAGAGAGGTGCGGACAGGGCAGACTTCCAGA 664
OY 70 ACCGCGTGGCCCCCATCTGACAGAGGTCAAACTGCTGCGCAGGTCACGATGCCAGCAAA 129
Db 665 ACCTGCACCTGCCCCCTGTGACAGACTGAAGTCTCATGACAGGTCATGCTCCCGCAGC 724
OY 130 CAGATCA 136
Db 725 AACCAACA 731

RESULT 14
US-09-188-930-262
: Sequence 262, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: TITLE OF INVENTION: and Methods For Their Use
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188.930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 262
: LENGTH: 1816
: TYPE: DNA
: ORGANISM: Mouse
US-09-188-930-262

Query Match
Best Local Similarity 55.9%; Score 37.4; DB 3; Length 1816;
Matches 71: Conservative 0; Mismatches 56; Indels 0; Gaps 0;

OY 10 CACGCTTGAGACTTCTAAAGAGACTTCGTGCGCGGGCGGTGCCGCTGCCGTCTCAAG 69
Db 605 CAGACGGGAGATGCTGTGAGGACGACCTGCTGCAGAGAGGTGCGGACAGGGCAGACTTCCAGA 664
OY 70 ACCGCGTGGCCCCCATCTGACAGAGGTCAAACTGCTGCGCAGGTCACGATGCCAGCAAA 129
Db 665 ACCTGCACCTGCCCCCTGTGACAGACTGAAGTCTCATGACAGGTCATGCTCCCGCAGC 724
OY 130 CAGATCA 136
Db 725 AACCAACA 731

RESULT 15
US-08-937-466-5
: Sequence 5, Application US/08937466
: Patent No. 5846779
: GENERAL INFORMATION:
: APPLICANT: Zhang, Ning
: APPLICANT: Amaral, M. Catherine
: APPLICANT: Chen, Jin-Long
: TITLE OF INVENTION: UCP3 Genes
: NUMBER OF SEQUENCES: 6

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-937-466-5

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Query Match 4.1%; Score 37; DB 2; Length 1777;
Best Local Similarity 52.2%; Pred. No. 0.44;
Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 728 GGAAGGGGCGGATTTATGTACACGGGACAGTGTGCGAGGAGATTGCCAAG 787
DB 682 GAACGTGAGGAGAGAGGAAATACAGAGGACTATGATGCTTACAGAACATCGCCAGGG 741
QY 788 ACGAAGAGCCAGGCTTCTTCAAAAGGTGCTGCCATGTCTCTGAGAGGATGGCG 847
DB 742 AGGAAGAGTCTAGAGGCGCTGTGGAAGGAGCTTGCCCAACATCACAAGAAATGCCATTG 801
QY 848 GTGCTTTGTATGCTGTGTATGATGATGATCAAAA 884
DB 802 TCACTGTGCTGAGATGCTGACCTAGACATCATCA 838

```

Search completed: June 22, 2003, 02:39:02
 Job Time : 57 secs


```

Oy      181  ATCCCTAAGACAGGGGCTTCCTCTCCTTTGGAGGGGAACCTGGCAACGTGATCCG  240
Db      181  ATCCCTAAGAGAGAGGGCTTCTCTCTCTCTGAGAGGGTAACCTGGCAACGTATCCG  240
Oy      241  TACTTCCCAACCCCAACCTCTCAACTTCCGCTTCAAGACAAGTACAAAGCAAGCTTCTTA  300
Db      241  TACTTCCCAACCCCAACCTCTCAACTTCCGCTTCAAGACAAGTACAAAGCAAGCTTCTTA  300
Oy      301  GGGGGGTGTGATCGCCATAAGCAGTTCTGGCGTACTTTGTGCTTAACCTGGCGTCCGGT  360
Db      301  GGGGGGTGTGATCGCCATAAGCAGTTCTGGCGCTACTTTGTGCTTAACCTGGCGTCCGGT  360
Oy      361  GGGGGCGGTGGGGCCACCTCCCTTTGGCTTTGTCTACCCGCTGACATTGGTAGACACAG  420
Db      361  GGGGGCGGTGGGGCCACCTCCCTTTGGCTTTGTCTACCCGCTGACATTGGTAGACACAG  420
Oy      421  TTGGCTGTGATGTGGGCGAGGGGGCGCCAGCGCTGAGTTCCATGGCTGGGGGACTGTATC  480
Db      421  TTGGCTGTGATGTGGGCGAGGGGGCGCCAGCGCTGAGTTCCATGGCTGTGGGCACTGTATC  480
Oy      481  ATCAAGATCTTCAAGTCTGATGGCCCTGAGAGGGGCTCTACAGAGGTTTCAACGTTCTGTC  540
Db      481  ATCAAGATCTTCAAGTCTGATGGCCCTGAGAGGGGCTCTACAGAGGTTTCAACGTTCTGTC  540
Oy      541  CAAGGCAATCTTATCTATGAGCTGCTACTTGGAGTCTATGATATCTCCCAAGGGATG  600
Db      541  CAAGGCAATCTTATCTATGAGCTGCTACTTGGAGTCTATGATATCTCCCAAGGGATG  600
Oy      601  CTGCGTGAACCCCAAGAACGTGCACATTTTGTGACTGTGATGATTTGCCCAAGTGTACG  660
Db      601  CTGCGTGAACCCCAAGAACGTGCACATTTTGTGACTGTGATGATTTGCCCAAGTGTACG  660
Oy      661  GCAGTGCAGAGGCTGCTCTCAACCCCTTTGACACTGTTGCTGTAGATGATGATGACAG  720
Db      661  GCAGTGCAGAGGCTGCTCTCAACCCCTTTGACACTGTTGCTGTAGATGATGATGACAG  720
Oy      721  TCCGGCGCGAAGGGCCCATATTTATGTACACGGGACAGTTGACTGCTGGAGAGATT  780
Db      721  TCCGGCGCGAAGGGCCCATATTTATGTACACGGGACAGTTGACTGCTGGAGAGATT  780
Oy      781  GCAAAAGACGAACGACCCAAAGGCTTCTCAAAAGTGCGTGCATATGTCTGAGAGGC  840
Db      781  GCAAAAGACGAACGACCCAAAGGCTTCTCAAAAGTGCGTGCATATGTCTGAGAGGC  840
Oy      841  ATGAGCGGTCTTTTGTATTGGTGTGTATGATGATCAAAAAATATCTCTAA  894
Db      841  ATGAGCGGTCTTTTGTATTGGTGTGTATGATGATCAAAAAATATGTCTAA  894

RESULT 2
US-09-811-094-1
: Sequence 1, Application US/09811094
: Patent No. US20010044144A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yazhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
: FILE REFERENCE: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: CURRENT APPLICATION NUMBER: US/09/811,094
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 894
: TYPE: DNA

```

Query Match		100.0%;	Score 894;	DB 10;	Length 894;
Best Local Similarity		100.0%;	Pred. No. 4.8e-287;		
Matches	894;	Conservative	0;	Mismatches	0;
				Indels	Gaps
OY	1	ATGGGTGATCAACGCTTGGAGCTTCCCTTAAGACACTTCTGCGCGGGGGCGTCCGCGTCC	60		
Db	1	ATGGGTGATCAACGCTTGGAGCTTCCCTTAAGACACTTCTGCGCGGGGGCGTCCGCGTCC	60		
OY	61	GTCCTCCAGACCGGGGTCCGCCCATGCGAGAGGGTCAACACTGCTCTCAGTCCAGAT	120		
Db	61	GTCCTCCAGACCGGGGTCCGCCCATGCGAGAGGGTCAACACTGCTCTCAGTCCAGAT	120		
OY	121	GCCAGCAACAGATACGTAGCTGAGAGACAGTACAAAGGATCATTTGATTGTGTGAGA	180		
Db	121	GCCAGCAACAGATACGTAGCTGAGAGACAGTACAAAGGATCATTTGATTGTGTGAGA	180		
OY	181	ATCCCTAAGAGACAGGCGCTTCTCTCTCTTGAGAGGGTAACTTGCCCAAGCTGATCCGT	240		
Db	181	ATCCCTAAGAGACAGGCGCTTCTCTCTCTTGAGAGGGTAACTTGCCCAAGCTGATCCGT	240		
OY	241	TACTTCCCCACCCAAAGCTCTCACTTGCCCTTCAAGGACAACTACACAGCTCTTTCTTA	300		
Db	241	TACTTCCCCACCCAAAGCTCTCACTTGCCCTTCAAGGACAACTACACAGCTCTTTCTTA	300		
OY	301	GGGGGTGAGATCCGATACAGTCTTGCGGGCTACTTGGCGGTAACTTGCGCGTCCGCT	360		
Db	301	GGGGGTGAGATCCGATACAGTCTTGCGGGCTACTTGGCGGTAACTTGCGCGTCCGCT	360		
OY	361	GGGGCGCGTGGGGCCACCTCCCTTGTGCTTCTTCTACCCGCTGAGCTTGTCTAGACACAG	420		
Db	361	GGGGCGCGTGGGGCCACCTCCCTTGTGCTTCTTGTCTACCCGCTGAGCTTGTCTAGACACAG	420		
OY	421	TTGGCTGCTGATGTGGGACAGCGCGGCCAGCGTGCATGGTCTGGGCGACTGTATC	480		
Db	421	TTGGCTGCTGATGTGGGACAGCGCGGCCAGCGTGCATGGTCTGGGCGACTGTATC	480		
OY	481	ATCAAGATCTTCAAGTCTGATGGGCTGAGGGGGCTTACGAGGGTTTCAAGCTCTCTGC	540		
Db	481	ATCAAGATCTTCAAGTCTGATGGGCTGAGGGGGCTTACGAGGGTTTCAAGCTCTCTGC	540		
OY	541	CAAGGACATTAATCTATAGAGCTGCTACTTCCGAGTCTATGATACTGCGCAAGGGGATG	600		
Db	541	CAAGGACATTAATCTATAGAGCTGCTACTTCCGAGTCTATGATACTGCGCAAGGGGATG	600		
OY	601	CTGCCCTGACCCCAAGAACGTGCACATTTTGTGAGCTGAGTGAATGCCAGAGTGTGACG	660		
Db	601	CTGCCCTGACCCCAAGAACGTGCACATTTTGTGAGCTGAGTGAATGCCAGAGTGTGACG	660		
OY	661	GCACTCGAGGGGTCTGCTCTTACCCTTTTACACACTTTCCTCGTAGAATGATGTGAG	720		
Db	661	GCACTCGAGGGGTCTGCTCTTACCCTTTTACACACTTTCCTCGTAGAATGATGTGAG	720		
OY	721	TCCGCGCCGAAGGGCGCATATTATGTACACGGGGACAGTTGACTCTGGAGAAAGATT	780		
Db	721	TCCGCGCCGAAGGGCGCATATTATGTACACGGGGACAGTTGACTCTGGAGAAAGATT	780		
OY	781	GCAAAAGACGAAGAGGCCAAGGCTTCTTCAAGAGTGGCTGCCAATGTCTGAGAGGC	840		
Db	781	GCAAAAGACGAAGAGGCCAAGGCTTCTTCAAGAGTGGCTGCCAATGTCTGAGAGGC	840		
OY	841	ATGGCGGTGCTTTTGTATTGGTGTGTGATGATGAGATCAAAAATATGTCTAA	894		
Db	841	ATGGCGGTGCTTTTGTATTGGTGTGTGATGATGAGATCAAAAATATGTCTAA	894		

```

: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleveland, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott M.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yashong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.420D3
: CURRENT APPLICATION NUMBER: US/09/810,644
: NUMBER OF FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 894
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-810-644-1

Query Match      100.0%: Score 894: DB 10: Length 894:
Best Local Similarity 100.0%: Pred. No. 4.8e-287:
Matches 894: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 ATGGGTGATCAGCCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCGTCCGCTGCC 60
Db 1 ATGGGTGATCAGCCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCGTCCGCTGCC 60
Oy 61 GTCTCCAGACCGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 61 GTCTCCAGACCGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Oy 121 GCAGCAACAGATCAGTCTGAGAGAGATCAAGAGGATCATGATGCTGGTGGAGA 180
Db 121 GCAGCAACAGATCAGTCTGAGAGAGATCAAGAGGATCATGATGCTGGTGGAGA 180
Oy 181 ATCCCTAAGGAGAGCGCTTCTCTCTCTCTGAGAGGAGTAACTGGCCCAAGTGAATCCG 240
Db 181 ATCCCTAAGGAGAGCGCTTCTCTCTCTCTGAGAGGAGTAACTGGCCCAAGTGAATCCG 240
Oy 241 TACTTCCCAACCGAGCTCTCAACTTCGCGCTTCAAGAGCAAGTCAAGAGCGTCTTCTTA 300
Db 241 TACTTCCCAACCGAGCTCTCAACTTCGCGCTTCAAGAGCAAGTCAAGAGCGTCTTCTTA 300
Oy 301 GGGGCTGGATGGGATTAAGCAAGCTTGGCGCTACTTTGCTGTAACCGTGGCGTCCGG 360
Db 301 GGGGCTGGATGGGATTAAGCAAGCTTGGCGCTACTTTGCTGTAACCGTGGCGTCCGG 360
Oy 361 GGGGCGCTGGGCGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 361 GGGGCGCTGGGCGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Oy 421 TTGGCTGTGATGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 421 TTGGCTGTGATGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Oy 481 ATCAAGATCTTCAAGTCTGATGGCGTGAAGGGGCTCTACAGAGGTTTCAACGCTCTCTG 540
Db 481 ATCAAGATCTTCAAGTCTGATGGCGTGAAGGGGCTCTACAGAGGTTTCAACGCTCTCTG 540
Oy 541 CAAGGATCATTTATATAGAGCTGCTACTTGGAGTATATATGCTGCAAGGGGATG 600
Db 541 CAAGGATCATTTATATAGAGCTGCTACTTGGAGTATATATGCTGCAAGGGGATG 600
Oy 601 CTGCTGACCCCAAGAGCGTCAATTTTGTGAGCTGATGATGCGCCAGAGTGTGACG 660
Db 601 CTGCTGACCCCAAGAGCGTCAATTTTGTGAGCTGATGATGCGCCAGAGTGTGACG 660
Oy 661 GCAGTGCAGAGGCTGTCTCTACCCCTTGTGACAGCTTGTGCTGATGATGATGACG 720
Db 661 GCAGTGCAGAGGCTGTCTCTACCCCTTGTGACAGCTTGTGCTGATGATGATGACG 720

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Oy 721 TCCGCGCGCAAGGCGCGCATTTATGTACAGCGGACAGTTGACTGCTGAGAGATTT 780
Db 721 TCCGCGCGCAAGGCGCGCATTTATGTACAGCGGACAGTTGACTGCTGAGAGATTT 780
Oy 781 GCAAAAGACGAGGAGCGGCGGCTTCTCAAGGCGCGGCGGCGGCGGCGGCGGCGG 840
Db 781 GCAAAAGACGAGGAGCGGCGGCTTCTCAAGGCGCGGCGGCGGCGGCGGCGGCGG 840
Oy 841 ATGGCGGCTGCTTTTGTATGTTGATGATGATGATGATGATGATGATGATGATGAT 894
Db 841 ATGGCGGCTGCTTTTGTATGTTGATGATGATGATGATGATGATGATGATGATGAT 894

RESULT 4
US-10-198-846-13437
: Sequence 13437, Application US/10198846
: Publication No. US2003009974A1
: GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Xu, Yongyao
: APPLICANT: Wang, Youzhen
: APPLICANT: Steilmann, Kathleen
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
: TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: FILE REFERENCE: MRI-049
: CURRENT APPLICATION NUMBER: US/10/198,846
: CURRENT FILING DATE: 2002-07-18
: PRIOR APPLICATION NUMBER: 60/306,220
: NUMBER OF SEQ ID NOS: 14084
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13437
: LENGTH: 1711
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1, 2, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405,
: LOCATION: 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415,
: LOCATION: 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425,
: LOCATION: 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434
: OTHER INFORMATION: n = A,T,C or G
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444,
: LOCATION: 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454
: OTHER INFORMATION: n = A,T,C or G
: US-10-198-846-13437

Query Match      97.7%: Score 873: DB 9: Length 1711:
Best Local Similarity 99.1%: Pred. No. 6.4e-280:
Matches 889: Conservative 0: Mismatches 5: Indels 3: Gaps 1:

Oy 1 ATGGGTGATCAGCCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCGTCCGCTGCC 60
Db 1 ATGGGTGATCAGCCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCGTCCGCTGCC 60
Oy 167 ATGGGTGATCAGCCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCGTCCGCTGCC 226
Db 167 ATGGGTGATCAGCCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCGTCCGCTGCC 226
Oy 61 GTCTCCAGACCGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 61 GTCTCCAGACCGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Oy 121 GCGAGCAACAGATCAGTCTGAGAGAGTCAAGAGGATCATGATGCTGGTGGAGA 180
Db 121 GCGAGCAACAGATCAGTCTGAGAGAGTCAAGAGGATCATGATGCTGGTGGAGA 180
Oy 287 GCGAGCAACAGATCAGTCTGAGAGAGTCAAGAGGATCATGATGCTGGTGGAGA 346
Db 287 GCGAGCAACAGATCAGTCTGAGAGAGTCAAGAGGATCATGATGCTGGTGGAGA 346
Oy 181 ATCCCTAAGGAGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 181 ATCCCTAAGGAGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Oy 347 ATCCCTAAGGAGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 406
Db 347 ATCCCTAAGGAGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 406
Oy 241 TACTTCCCAACCGAGCTCTCAACTTCGCGCTTCAAGAGCAAGTCAAGAGCGTCTTCTTA 300
Db 241 TACTTCCCAACCGAGCTCTCAACTTCGCGCTTCAAGAGCAAGTCAAGAGCGTCTTCTTA 300

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Db	407	TACTTCCCAACCAAGCTCTCACTTGGCCCTTCAAGACAGACAGTACACAGCTCTTTCTTA	466
Oy	301	GGGGGTGTGATTCGGCATMAAGCAGTTCCTGGCGCTACTTTGCTGTGAATACGCGCTCCGGT	360
Db	467	GGGGGTGTGATTCGGCATMAAGCAGTTCGGCGCTACTTTGCTGTGAATACGCGCTCCGGT	526
Oy	361	GGGGCGCGTGGGGCCACCTCCCTTTGCTTTGTCTAACCGCTGAGACTTTGCTAACGACGAG	420
Db	527	GGGGCGCGTGGGGCCACCTCCCTTTGCTTTGTCTAACCGCTGAGACTTTGCTAACGACGAG	586
Oy	421	TTGGCTGTGATGTGGGAGGCG---CCGCCAGCGCTGAGTTGCATGGTCTGGGGACAGT	477
Db	587	TTGGCTGTGATGTGGGAGGCGCGCGCCCGCCAGCGCTGAGTTGCATGGTCTGGGGACAGT	646
Oy	478	ATCATCAAGATCTTCAACGTCTGATGGCTGAGGGGGCTCTACAGAGGTTTCAACGCTCTCT	537
Db	647	ATCATCAAGATCTTCAACGTCTGATGGCTGAGGGGGCTCTACAGAGGTTTCAACGCTCTCT	706
Oy	538	GTCCAGGATCATTTATTTATAGAGCTGCCCTACTTGGAGTCTATGATACTGGCAAGGGG	597
Db	707	GTCCAGGATCATTTATTTATAGAGCTGCCCTACTTGGAGTCTATGATACTGGCAAGGGG	766
Oy	598	ATGCTGCTGACCCCAAGACGCTGACATTTTTTGGAGCTGGATGGATTTGCCAGAGCTGTG	657
Db	767	ATGCTGCTGACCCCAAGACGCTGACATTTTTTGGAGCTGGATGGATTTGCCAGAGCTGTG	826
Oy	658	ACGGCAGTGGAGGGCTGCTGCTTACCCCTTGTGACACTGTTTGTGCTGATGATGTGATG	717
Db	827	ACGGCAGTGGAGGGCTGCTGCTTACCCCTTGTGACACTGTTTGTGCTGATGATGTGATG	886
Oy	718	CAGTCCGGCCGGAAAGGGGCGGATTTATGTACACGGGGACAGTTGACTGCTGGAGAGAG	777
Db	887	CAGTCCGGCCGGAAAGGGGCGGATTTATGTACACGGGGACAGTTGACTGCTGGAGAGAG	946
Oy	778	ATTGCAAAAGACGAAGAGCCAAAGGCTTTCTTCAAGAGTGCCTGGTCAATGTCTGAGA	837
Db	947	ATTGCAAAAGACGAAGAGCCAAAGGCTTTCTTCAAGAGTGCCTGGTCAATGTCTGAGA	1006
Oy	838	GGCATGGCGGCTCTTTTGTATTGGTGTGTATGATGATCAAAAATATGTCTAA	894
Db	1007	GGCATGGCGGCTCTTTTGTATTGGTGTGTATGATGATCAAAAATATGTCTAA	1063

RESULT 5

```

Sequence 1377, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIORITY APPLICATION NUMBER: US 60/222,040
PRIORITY FILING DATE: 2000-07-31
PRIORITY APPLICATION NUMBER: US 60/222,880
PRIORITY FILING DATE: 2000-11-02
PRIORITY APPLICATION NUMBER: US 60/290,029
PRIORITY FILING DATE: 2001-05-11
PRIORITY APPLICATION NUMBER: US 60/290,645
PRIORITY FILING DATE: 2001-05-15
PRIORITY APPLICATION NUMBER: US 60/292,336
PRIORITY FILING DATE: 2001-05-22
PRIORITY APPLICATION NUMBER: US 60/295,798
PRIORITY FILING DATE: 2001-06-06
PRIORITY APPLICATION NUMBER: US 60/297,457
PRIORITY FILING DATE: 2001-06-13
PRIORITY APPLICATION NUMBER: US 60/298,884

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: PRIOR FILING DATE: 2001-06-19
 : PRIOR APPLICATION NUMBER: US 60/303,459
 : PRIOR FILING DATE: 2001-07-09
 : NUMBER OF SEQ ID NOS: 1740
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1327
 : LENGTH: 1196
 : TYPE: DNA
 : ORGANISM: Rattus norvegicus
 : FEATURE:
 : OTHER INFORMATION: Genbank Accession No. US20020119462A1 D12770
 : US-09-917-800A-1327

Query Match	84.88	Score 757.8	DB 10	Length 1196
Best Local Similarly	91.18	Pred. No. 1.2e-241		
Matches 817	Conservative	0	Mismatches 77	Indels 3
				Gaps 1

OY	1	ATGGGATATCAACGCTTGGAGCTTCTCTTAAGAGACTTCTGCGCGGGGCGGCTGCCCGCTGCC	60	
Db	76	ATGGGGGATATGAGCTTTTGAGGCTTCTTAAGAGACTTCTGCGAGAGGTGGGATGCCCGCGCC	135	
OY	61	GTCCTCAAGAACCGGGGTCGCCCCATCGAGAGGGGTCAAACTGCTGCTCAGGTCCAGCAT	120	
Db	136	GTCCTCAAGAACCGGGGTCGCCCCATCGAGAGGGGTCAAACTGCTGCTCAGGTCCAGCAT	195	
OY	121	GCCAGCAAAACAGATCAGTGTGAGAGAGCAGTACAAGAGGATCATTTGATGTGTGTGAGA	180	
Db	196	GCCAGCAAAACAGATCAGTGTGAGAGAGCAGTACAAGAGCATTTGATGTGTGTGAGA	255	
OY	181	ATCCCTTAAGAGAGCAGGGCTTCTCTCTCTTGAGAGGGGTAACTGTGGCCACGTATCCGT	240	
Db	256	ATCCCTTAAGAGAGCAGGGCTTCTCTCTCTTGAGAGGGGTAACTGTGGCCACAGTATCCGG	315	
OY	241	TACTTCCCAACCCAGCTCTCAACTTGCCTTCAAGGACAGTACAAGCAGCTCTTCTTA	300	
Db	316	TACTTCCCAACCCAGCTCTCAACTTGCCTTCAAGGACAGTACAAGCAGATTTTCTCTG	375	
OY	301	GGGGGTGTGATCGGCATTAAGCAGTTTGGCGCTACTTTCGTGTTAACTTGGCTCCGGT	360	
Db	376	GGAGGTGTGATCTCTCATTAAGCAGTTTGGGGCTACTTCCCTGTAACTGGCTCTGGT	435	
OY	361	GGGGCGCTGGGGGCACCTCCCTTGGTTTGTACCGCGGGGACTTTGCTAAGAGACAGG	420	
Db	436	GGGGCAGCTGGGGCTACCTCCCTTGGTTTGTCTTACCGCACTGGACTTGTGAGAGACAGG	495	
OY	421	TTGGCTCTGATGTGGGCAAGCG---GCCCGAGCGTAGTTCCATGTGCTTGGGCGAGCTGT	477	
Db	496	CTGGCTCTCGACGTGGGCAAGGAGTCTTCCAGCGTAGTTCAATGGGCTGGGTGACTGT	555	
OY	478	ATCATCAAGATCTTCAAGTGTGATGGCTGAGGGGCTCTAACGCGTTTCAACGCTCT	537	
Db	556	CTCACCAAGATCTTCAAGTGTGATGGGCTCAAGGGCTCTAACGCGTTTCAAGCTCTCT	615	
OY	538	GTCCAAAGCATATTAATTAAGAGCGGCTACTTGGAGAGCTGTGATPACTGGCCAAAGGG	597	
Db	616	GTCCAGAGGCAATCATCTATACAGAGCTGCTACTTCCGAGCTTATGACACTGCCAAAGGGG	675	
OY	598	ATGCTGCCCTGACCCCAAGAGCTGCACATTTTCTGAGCTGGATGATTGCCAAGCTGTG	657	
Db	676	ATGCTGCCAGACCCCAAGATGTGCACATTAATTGTGAGTGTGATGATTGCCAAGAGTGTG	735	
OY	658	ACGGCAGTCCGAGGGCTGCTGTCTCAACCCCTTTGACACGTGTGTGCTTACAAATGATGATG	717	
Db	736	ACAGCCCTGGCGGGGCTGTCTTATCACTTTGACACTCTCCGTCTAGAGTATGATG	795	
OY	718	CATCTCCGCGCGGAAGGGGCGGATTAATTAATTAACACGGGACAGTTGACTCTGGAGAGAG	777	
Db	796	CAGTCTGGCGGAAAGGGCTGATTAATTAATTAACACGGGACAGTTGACTCTGTGAGAGAG	855	
OY	778	ATTTCGAAAAGCAGAGGACCCAAAGCCCTTTCGAAAGGTGCTGGTCCCAATGTGCTGAGA	837	
		856	ATTTCGAAAAGTATAGAGACCAAGCTTTCTTCAAGAGTCTTGGTCTTCAAGCTACTGAGA	915

QY 838 GGCATGGCGCTTTTGTATGTTGATGATGATCAAAAATATGCTTAA 894
 DB 916 GGCATGGCGGCTTTTGTATGTTGATGATGATGATCAAAAATATGCTTAA 972

RESULT 6
 US-09-185-904A-3

? Sequence 3, Application US/09185904A
 ? Patent No. US20020177185A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Anderson, Christen M.
 ? APPLICANT: Davis, Robert E.
 ? APPLICANT: Cleverger, William
 ? APPLICANT: Wiley, Sandra Eileen
 ? APPLICANT: Miller, Scott W.
 ? APPLICANT: Szabo, Tomas R.
 ? APPLICANT: Ghosh, Soumitra S.
 ? TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ? TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 ? FILE REFERENCE: 660088, 420
 ? CURRENT APPLICATION NUMBER: US/09/185, 904A
 ? CURRENT FILING DATE: 1998-11-03
 ? NUMBER OF SEQ ID NOS: 33
 ? SOFTWARE: FastSeq for Windows Version 3.0
 ? SEQ ID NO 3
 ? LENGTH: 897
 ? TYPE: DNA
 ? ORGANISM: Homo sapien
 ? US-09-185-904A-3

Query Match 63.1%; Score 564.2; DB 9; Length 897;
 Best Local Similarity 77.6%; Pred. No. 2.9e-177;

Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

QY 1 ATGGGTGATCAGCGCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCTGCGCGCTGCG 60
 DB 1 ATGAGGAGACAGCGCTTCTTCTGCGCGCGGCTTCTTGGCGGAGCATGCGCGCGCG 60
 QY 61 GTCTCCAGACCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 61 ATCTCCAGACCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 QY 121 GCGAGCAACAGATGCTGCTGAGAGAGGATCAAGAGGATCATTTGCTGCTGAGA 180
 DB 121 GCGAGCAACAGATGCTGCTGAGAGAGGATCAAGAGGATCATTTGCTGCTGAGA 180
 QY 181 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGATCAAGAGGATCATTTGCTGCTG 240
 DB 181 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGATCAAGAGGATCATTTGCTGCTG 240
 QY 241 TACTTCCCACTCAAGCGCTCAACTTCCGCTTCAAGAGATCAAGAGATCTTCTG 300
 DB 241 TACTTCCCACTCAAGCGCTCAACTTCCGCTTCAAGAGATCAAGAGATCTTCTG 300
 QY 301 GGGGGTGTGATGCTGATGAGGATGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 301 GGGGGTGTGATGCTGATGAGGATGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 361 GGGGGTGTGATGCTGATGAGGATGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 GGGGGTGTGATGCTGATGAGGATGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 TTGGCTGTGATGCTGATGAGGATGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCT 477
 DB 421 TTGGCTGTGATGCTGATGAGGATGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCT 477
 QY 478 ATCATCAAGATCTTCAAGTCTGATGAGGATGCTGAGGAGGCTTCAAGAGGCTTCT 537
 DB 478 ATCATCAAGATCTTCAAGTCTGATGAGGATGCTGAGGAGGCTTCAAGAGGCTTCT 537
 QY 538 GTCCAGGATCATTTATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
 DB 538 GTCCAGGATCATTTATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597

DB 541 GTGAGGAGCATCATATACCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 598 ATGCGGCGGAGCG 657
 DB 601 ATGCGGCGGAGCG 660
 QY 658 ACGGAGGCGGAGCG 717
 DB 661 ACGGAGGCGGAGCG 720
 QY 718 CAGTCCGCGGAGCG 777
 DB 721 CAGTCCGCGGAGCG 780
 QY 778 ATTCGAAAAG 837
 DB 781 ATTCGAAAAG 840
 QY 838 GGCATGGCGGCTTTTGTATGTTGATGATGATCAAAAATATGCTTAA 894
 DB 841 GGCATGGCGGCTTTTGTATGTTGATGATGATCAAAAATATGCTTAA 897

RESULT 7
 US-09-811-094-3

? Sequence 3, Application US/09811094
 ? Patent No. US2001004414A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Anderson, Christen M.
 ? APPLICANT: Davis, Robert E.
 ? APPLICANT: Cleverger, William
 ? APPLICANT: Wiley, Sandra Eileen
 ? APPLICANT: Miller, Scott W.
 ? APPLICANT: Szabo, Tomas R.
 ? APPLICANT: Ghosh, Soumitra S.
 ? APPLICANT: Moos, Walter H.
 ? APPLICANT: Pei, Yezhong
 ? TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
 ? TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 ? FILE REFERENCE: 660088, 420D4
 ? CURRENT APPLICATION NUMBER: US/09/811, 094
 ? CURRENT FILING DATE: 2001-03-14
 ? NUMBER OF SEQ ID NOS: 37
 ? SOFTWARE: FastSeq for Windows Version 3.0
 ? SEQ ID NO 3
 ? LENGTH: 897
 ? TYPE: DNA
 ? ORGANISM: Homo sapien
 ? US-09-811-094-3

Query Match 63.1%; Score 564.2; DB 10; Length 897;
 Best Local Similarity 77.6%; Pred. No. 2.9e-177;

Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

QY 1 ATGGGTGATCAGCGCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCTGCGCGCTGCG 60
 DB 1 ATGAGGAGACAGCGCTTCTTCTGCGCGCGGCTTCTTGGCGGAGCATGCGCGCGCG 60
 QY 61 GTCTCCAGACCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 61 ATCTCCAGACCGCGGCTGCTGCTGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 121 GCGAGCAACAGATGCTGCTGAGAGAGGATCAAGAGGATCATTTGCTGCTGAGA 180
 DB 121 GCGAGCAACAGATGCTGCTGAGAGAGGATCAAGAGGATCATTTGCTGCTGAGA 180
 QY 181 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGATCAAGAGGATCATTTGCTGCTG 240
 DB 181 ATCCCTAAGAGAGAGGCTTCTCTCTGAGAGGATCAAGAGGATCATTTGCTGCTG 240
 QY 241 TACTTCCCACTCAAGCGCTCAACTTCCGCTTCAAGAGATCAAGAGATCTTCTG 300
 DB 241 TACTTCCCACTCAAGCGCTCAACTTCCGCTTCAAGAGATCAAGAGATCTTCTG 300

Query Match	63.18;	Score 564.2;	DB 10;	Length 897;
Best Local Similarity	77.68;	Pred. No. 2.9e-177;		
Matches 696;	Conservative 0;	Mismatches 198;	Indels 3;	Gaps 1

OY	1	ATGGGTGATACAGCTTGGAGCTTCCGTAAGAGACTTCCTGGCCGGGGCGGGTCCGCTGC	60
OY	1	ATGACGGAGACAGGCCCATCTCTCTTCCGCAAAAGACTTCTTGGCCGAGGACATCGCCGCCGCC	60
OY	61	GTCTCCAAAGACCCGGGTGCGCCCATATCGAAGGGGTCAAACTGCTGCTGCAGGTCCAGCAT	120
OY	61	ATCTCCAAAGACGGCGGTGGCTCGCATCGAAGCGGGTCAACCTGCTGCTCCAGGTCCAGCAC	120
OY	121	GCCAGCAAAACAGATCAGTGTCTAGAAGCAGTACAAAGCATCTATTGATGTGTGTGAGA	180
OY	121	GCCAGCAAAACAGATCGCCGCCGACAAGCAGTACAAAGGCATCTGTGACATCTTGTCCGC	180
OY	181	ATCCGTAAGGAGCAGGGGCTTCCCTCCCTCTGAGGGGGTAACTGGCCCAAGCGATCCGT	240
OY	181	ATCCCCAAGAGCAGGGGCTGCTGTCTCTTCTGAGGGGCAACCTTCCCAACGTCATTTCCG	240
OY	241	TACTTCCCAACCCAGACTTCACATTCGCGCTTCAAGAGCAAGTACAGACAGCTCTTCTTA	300
OY	241	TACTTCCCAACCCAGACTTCACATTCGCGCTTCAAGAGTAAAGTACAGACAGATCTTCTCG	300
OY	301	GGGGGTGTGGATCGGCATTAAGCAGTTCTGGCGCTACTTTGTGTAACTGGCGTCCGGT	360
OY	301	GGGGCGGTGGACACACACAGCAGTCTGGAGGTACTTTGCGGGCAACCTGCGCTCCGC	360
OY	361	GGGGCGGCGTGGGGCCACTCCCTTCCCTTGTCTACCCGCTGACATTTGTTAGACACAG	420
OY	361	GGTGTGGCGCGCGCACCTCCCTCTCTTCTGTACCCCTGTGATTTTGTCCAAACCCGC	420
OY	421	TTCGCTGCTGATGTGGGCGAG--CGCGCCACCGCTGAGTTCATGGTCTGGCGCACTGT	477
OY	421	CTGGCAGCGGACGTGGGAAGTCAAGCACAGAGCGGAGTTCCGAGGCTGGGAGACTGC	480
OY	478	ATCATCAAGATCTTCAAGTCTGATGGCCCTGAGGGGCTCTTACAGGGCTTTCACAGTCTCT	537
OY	481	CTGTGAAGATCACCAAGTCCGACGGCATCCGGGCGCTTACCAAGGCTTCAAGTCTCC	540
OY	538	GTCCAAAGCATATATATCTATAGAGCTGCTACTTGGAGTCTATATACTGCCAAGGG	597
OY	541	GTGCAAGGGCATATCATCTTACCGGGGCGCTTACTTGGCGTGTACGATACGGCCAAAGGC	600
OY	598	ATGCTGCGTACCCCAAGAGCGTGCACATTTTTGTAGCTGATGATATGGCCAGAGTGT	657
OY	601	ATGCTGCCGACCCCAAGAACACGCACTGTGTGTAGCTGGATGTATCGCGACACCCTG	660
OY	658	ACGCGAGTGCAGGGGCTGCTGTCTTACCCCTTTGACACTGTTCGTGTAGATGATGAT	717
OY	661	ACGGCGGTGGCGGGGTGTGTCTTACCCCTTTCGACAGCGGTGGCGGCGCATGATGATG	720
OY	718	CAGTCCGGCCGAAGGGGCCATATATATGACAGGGGACAGTACTGCTGAGGAG	777
OY	721	CAGTCCGGCCGAAGAGACCTGACATCATGTACACGGGACCGTCCGATGTTTGGAGGAG	780
OY	778	ATTGCAAAAGACGAAGGAGCGACTTCTTCAAGAGGCGCGTGTCCAAATGTGCTGAGA	837
OY	781	ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAGAGGTCGGGTCCAAAGTCTGCGG	840
OY	838	GCGATCGCGCGGTCTTTGTATTTGATGTGTATGATGATGATCAAAAAATATGTCTAA	894
OY	841	GCGATGGGGGGCGCTTCTGCTGTGTGCTGTACGAGACCTCAAGAAAGGTGATCTAA	897
RESUL 9			
US-10-037-270-687			
: Sequence 687, Application US/10037270			
: Publication No. US20030104529A1			
: GENERAL INFORMATION:			
: APPLICANT: Tang, Y. Tom			
: APPLICANT: Liu, Chenghua			
: APPLICANT: Asundi, Vinod			
: APPLICANT: Zhang, Jie			
: APPLICANT: Ren, Peiyun			
: APPLICANT: Chen, Rui-hong			
: APPLICANT: Zhao, Qing A.			


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Db      | 101 GGTGCTGTGGACAAAGAACCCAGTTTGGCCCTACTTTGGCAGAGGAATGTGCATTCGGCT   360
Oy      | 361 GGGCGCGCTGGGGCCACCCTCTTTCCTTTGTCTACCCGCTGGACTTTGCTAGGACCAG   420
Db      | 361 GGTCGCCGACGAGGCCACCATCTGTTTGTGTGGTAACCCCTTGATTTTCCCGTACCCTG   420
Oy      | 421 TTGGCTGCTGANTGTGGCCA---GGCGGCCCCAGCGTGAATTCATGTGCTGGCGCACTGT   477
Db      | 421 CTACGAGCTGATGTGGGTAAAGCTGGACTGGACAAGAGGAAATTTCCGAGGCCCTCGGTGACTGC   480
Oy      | 478 ATCATCAGATCTTCAACTGTGATGGCTGAGAGGGGCTCTACAGAGGCTTTCACAGCTCTCT   537
Db      | 481 CTGGTTAAGATCTTCAAATCTGTATGTGGATAAAGGCCCTGTACCAAGGCTTTAAGCTGTCT   540
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Db      | 541 GTGCAAGGCTATTATCATCTTACCGACCCCGCTACTTCGGATCTATGACACTGCAAGAAGGA   600
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Oy      | 658 ACGGACAGTGCAGAGGCTCTGTCCTACCCCTTTTGACACTGTTTCGTGTAGAAATGATGATC   717
Db      | 661 ACTGCTGTTCGCGGGTGTACTTCTATCCATTTTGAACACCGCTTCCGCGCGCATGATGATG   720
Oy      | 718 CAGTCCGCGCCGAAAGGGCGCATTTTATGTACAGGGGACAGTGTGACTGTGGAGGAAG   777
Db      | 721 CAGTCAGGGCCCAAGAAAGCACTGACATCTACACAGGACACCTTGACCTGCGCGCGAAG   780
Oy      | 778 ATTGCAAAAAGCAGAGAGCACCAGGSCCTTCTTCAAGAGCGCTGGTCCAAATGCTGAGAG   837
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Oy      | 838 GC CATGGCGCGCTCTTTTGTATTGGTGTGTATGATGATGAGATCAAAAAATATGTCTAA   894
Db      | 841 GCGATCGCTGCTGCTTTTGTGCTTCTTGTATGATGAATCAAGAACTACACATATA   897

RESULT 11
US-09-811-094-2
: Sequence 2, Application US/09811094
: Patent No. US2001004414A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleverger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pei, Yashong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
: FILE REFERENCE: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: CURRENT APPLICATION NUMBER: US/09/811,094
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 897
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-811-094-2
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Query Match	61.9%	Score 553	DB 10	Length 897
Best Local Similarity	76.8%	Pred. No. 1.6e-173		
Matches 689	Conservative	0	Mismatches 205	Indels 3
				Gaps 1

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Oy 61 GTCTCCAGAGACCCGGGTGCGCCCCCATTCGAGAGGTCAAACTGCTGCTGCAGGTCCAGAT 120

Db 61 ATCTCCAGAGACGGCGGTAGCGCCCTCGAGCGGGGTCAACGCTCTGCTCGCAGGTGCGAGAT 120

Oy 121 GCCACCAAAACAGATACGTGCTGAGAAAGCATCAAAAGGATCATATGATGTGTGGTGACA 180

Db 121 GCCACCAAGCAATACGTACGACATATAGCAATCAAAAGGATTTATAGACTGCGGTGTCCT 180

Oy 181 ATCCCTAAGAGACAGGCGTCTCTCTCTCTTGAGGGGTGTAACCTGGCCCAAGCTGATCCGT 240

Db 181 ATTCCCAAGAGACAGGAAGTCTGTGTCCTTCGTGGCGGGTAACCTGGCCCAATGATCATACA 240

Oy 241 TACTTCCCACCAACGCTCTCACTTCCGCTTCAAGAGACAAGTACAGACGCTCTTCTTA 300

Db 241 TACTTCCCACCAACGCTCTTAACTTCGCTTCAAAAGATAATACAAAGCAGATCTCTCTG 300

Oy 301 GGGGGTGTGATCGGCATTAAGCAGTTCTGGGCTCACTTGTGCTGTAACCTGGGCGTCCGGT 360

Db 301 GGTGTGTGTGACAAAGAACCCAGATTTTGGCCCTACTTTGCAAGGAATCTGGCATGGGT 360

Oy 361 GGGGCGCTGGGGCCACCTCTCCCTTTGCTTTGCTACCCGCTGACATTTGCTAGACACAG 420

Db 361 GGTGCGCAGGGGCCACATCCTCTGTGTTTGTGTACCCCTTGATTTTGGCCGTACCCGT 420

Oy 421 TTGGCTGCTGATGTGGCA---GGCGCGCCACGCTGATTCATGCTGTGGGCACTGT 477

Db 421 CTAGCAGCTGATGTGGGTAAAGCTGAGCTGAAGGGAATTCGAGGCGCTCGGTGACTGC 480

Oy 478 ATCATCAGAGATCTTCAAGCTGATGGCTGAGAGGGGCTTACACAGGTTTCAACGCTGCT 537

Db 481 CTGTGTAAGATTCACAAATCTGATGGATTAAAGGCGCTGTACCAGGCTTTAAAGCTGCT 540

Oy 538 GTCCAAAGCACTATTATCTATAGACCTGCTACTTTCGAGTCTATCATCTGCCAAGCGG 597

Db 541 GTGCGGGTATTATATCTATACGACCGGCTACTTCGCTATCTATGACACTGCCAAAGGA 600

Oy 598 ATGCGGCGTGAACCCCAAGAGCTGCACATTTTGTGAGCTGGATCATATGCCAGAGTGG 657

Db 601 ATGCTTCGGATGCCCAAGACACTACATCGTCACTGCTGGATGATGCCACAGACTGTTC 660

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Db 781 ATTGCTGCTGATGAAGGAGGCAAACTTTTTCAGAGGTGCATGTGTCCAATGTTCACAA 840

Oy 838 GGCATGGCGGCTGTTTGTATGTGTGTTATGATGATGATCAAAATAATGTCTTA 894

Db 841 GGCATGGGTGTGCTTTGTGCTGCTCTTGTATGATGATGAATCAAAAGTACACATTA 897

RESULT 12
US-09-810-644-2
: Sequence 2, Application US/09810644
: Patent No. US20020012992A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clewenger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yazhong

;; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
;; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
;; FILE REFERENCE: 660088.420D3
;; CURRENT APPLICATION NUMBER: US/09/810.644
;; CURRENT FILING DATE: 2001-03-14
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 897
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-810-644-2

Query Match 61.9% Score 553; DB 10; Length 897;
Best Local Similarity 76.8%; Pred. No. 1.6e-173;

Matches 689; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Cy 1 ATGGGATATACAGCTTTGGAGCTTCTTAAGAGCTTCCGCGCGGCGCGGCGCGCTCC 60
Db 1 ATGAGAGATGGCGGATTTCTCTGCGCAAGAGACTTCTGGGAGAGTGGAGTGGCGCGC 60
Cy 61 GTCTCCAGAGCGCGGCTGCGCCCATCGAGAGGTCATGCTGCTGCGAGTCCAGCAT 120
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Cy 121 GCCAGCAACAGATGCTGCTGAGAGAGTACAAAGGATCATGATTGCTGCTGAGA 180
Db 121 GCCAGCAACAGATGCTGCTGAGAGAGTACAAAGGATCATGATTGCTGCTGCTGCT 180
Cy 181 ATCCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGCTTAACCTGCGCAACGTCATCCGT 240
Db 181 ATTCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGCTTAACCTGCGCAACGTCATCCGA 240
Cy 241 TACTTCCCGCCAGAGCTCTCACTTCCCTTCAAGAGAGTACAGAGAGCTCTTCTTA 300
Db 241 TACTTCCCGCCAGAGCTCTCACTTCCCTTCAAGAGAGTACAGAGAGTCTTCTG 300
Cy 301 GGGGGTGTGATCGGCTAAGAGAGTTCGGGCTCTTGGCTGATGCTGCGCGCGGT 360
Db 301 GGTGGTGTGAGAGAGAGAGAGAGAGTTCGGGCTCTTGGAGAGAGTTCGCGCGGT 360
Cy 361 GGGGCGCTGGGCGCGCGCGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 GGTGGCGGAGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Cy 421 TTGGCTGTGATGTGGCA---GGCGCGCGAGCGTGAAGTTCATGCTGCGCGCTGT 477
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Cy 478 ATCATCAGATCTTCAAGCTGATGAGGCGCTGAGAGGCGCTGAGAGGCTTCAAGCTCT 537
Db 481 CTGGTTAGATCTTCAAACTGATGAGGCGCTGAGAGGCGCTTCAAGCTGCT 540
Cy 538 GTCCAGGATCATATATATATAGAGAGCTGCTACTTCCGAGTCTATGATAGTCCAGAGG 597
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Cy 718 CAGTCCGCGGAGAGGCGGCTATATATAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCT 777
Db 721 CAGTCCGCGGAGAGAGAGAGAGAGAGTATATATAGAGAGAGCTGCTGCTGCTGCTGCT 780
Cy 778 ATTGCAAGAGAGAGAGAGAGAGGCTTCTTCAAGAGTGCCTGCTGCTGCTGCTGCTGCT 837
Db 781 ATTGCTGATGAGAGAGAGAGAGAGCTTTTTCAGAGGCTGCTGCTGCTGCTGCTGCTGCT 840

Cy 838 GGCATGGCGGCTGCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
Db 841 GGCATGGCGGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

RESULT 13

US-10-044-090-152

Sequence 152; Application US/10044090

Patent No. US20020137081A1

GENERAL INFORMATION:

APPLICANT: Olga Bandman

TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVA

FILE REFERENCE: PA-0028 US

CURRENT APPLICATION NUMBER: US/10/044.090

CURRENT FILING DATE: 2002-01-09

NUMBER OF SEQ ID NOS: 850

SOFTWARE: PERL Program

SEQ ID NO 152

LENGTH: 2592

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc-feature

OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11

NAME/KEY: unsure

LOCATION: 1131, 1929

OTHER INFORMATION: a, t, c, g, or other

US-10-044-090-152

Query Match 60.6% Score 542.2; DB 12; Length 2592;
Best Local Similarity 77.4%; Pred. No. 1e-169;

Matches 696; Conservative 0; Mismatches 198; Indels 5; Gaps 3;

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Db 207 ATGAGAGATGGCGGATTTCTCTGCGCAAGAGACTTCTGGGAGAGTGGAGTGGCGCGC 266
Cy 60 GGTGCAAGAGCGGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118
Db 267 CATCTCCAGAGAGCG 326
Cy 119 ATCCAGCAACAGATGCTGAGAGAGTACAGAGAGTCAATGCTGCTGCTGCTGCTGCT 178
Db 327 ACGGAG 386
Cy 179 GATTCCTAAG 238
Db 387 GCATCCCAAG 446
Cy 239 GTTACTTCCCGCCAGAGCTGCTCAAGCTTCCGCTTCAAGAGAGAGAGAGAGAGAGAG 298
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Cy 299 TAGGGGAG 358
Db 507 TGGGGGAG 566
Cy 359 GTGGGCGGCTGGGCG 418
Db 567 GCGGCGGCGGCG 626
Cy 419 GGTGGCTGCTGATGTGGGAG---CGCGCGCGAGAGTTCATGCTGCTGCTGCTGCTGCT 475
Db 627 GCGGCGAGCGGAGCTGGGAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 686
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Db 687 GCGTGTGAGAGATGAG 746
Cy 536 CTGTCCAGAGAGATCATATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
Db 747 CCGTCCAGAGAGATCATATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806

GenCore version 5.1.6
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(Without alignments)
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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_estl:*
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26: em_gss_pro:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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9	681.2	76.2	879	13	B1458358
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11	670.4	75.0	907	13	B1667026
12	665.8	74.5	862	14	B0214399
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24	629.8	70.4	863	13	B1408467
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33	607.6	68.0	757	13	B1092477
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37	604.4	67.6	928	9	AL578737
38	601.4	67.3	741	13	B1669668
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41	597	66.8	721	14	B0548008
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ALIGNMENTS

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DEFINITION mRNA sequence.
ACCESSION BG673955
VERSION BG673955.1 GI:13905347
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 964)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: L1AM10592 row: d column: 07
High quality sequence stop: 835.
Location/Qualifiers
1..964
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 188 a 249 c 310 g 217 t
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Query Match 85.2% Score 761.4; DB 12; Length 964;
Best Local Similarity 95.2% Pred. No. 3.7e-202;
Matches 829; Conservative 0; Mismatches 36; Indels 6; Gaps 4;
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152 GTCTCCAGAGCCGGCGTCCCGCATCGAGAGGTCACAACTGCTGTCAGTCAGCAT 211
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|||||
212 GCCAGCAACAGATCAGTGTGAGAGGATCAAAAGGATCATGATTGTGTGTGAGA 271
181 ATCCCTAAGAGCAGAGGCTTCTCTCTCTGAGAGGGTAACTGGCCCACTGATCCGT 240
272 ATCCCTAAGAGCAGAGGCTTCTCTCTCTGAGAGGGTAACTGGCCCACTGATCCGT 331
241 TACTTCCCAAGCAAGCTCTCACTTCCCTTCAAGAGCACTACAGAGCTTTCTTA 300
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332 TACTTCCCAAGCAAGCTCTCACTTCCCTTCAAGAGCACTACAGAGCTTTCTTA 391
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871 AATTG-GAAGAGCAAGAGAGCCAGGCTTCTTCAAGAGTGGCTGCTCAATGTCTGAG 929
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Db 930 GAGGCATGAGAGGCTTATAGATCGCGTATG 960
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ACCESSION AL556492
VERSION AL556492.1 GI:12899215
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
location/Qualifiers
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/clone_lib="LTI.NFL006.PL2"
/tissue="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 164 a 229 c 271 g 194 t 1 others
ORIGIN
Query Match 82.7% Score 739.6; DB 9; Length 859;
Best Local Similarity 98.8% Pred. No. 4.5e-196;
Matches 765; Conservative 1; Mismatches 5; Indels 3; Gaps 2;
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|||||
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61 GTCTCCAGAGCCGGCGTCCCGCATCGAGAGGTCACAACTGCTCAGAGTCAGCAT 120
|||||
147 GTCTCCAGAGCCGGCGTCCCGCATCGAGAGGTCACAACTGCTCAGAGTCAGCAT 206
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387 GGGGGTGTGATCGGATATAGCATTTGGGGCTTCTTGGTGAACCTGGCGCGGT 446
361 GGGGGCTGTGGGGCAGCTCCCTTGTCTTGTGATCCGCGTGAACCTTTGTAGAGCAGG 420

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447 GGGGGCGCTGGGGCCACTCCCTTGTCTTGTCTACCCGCTGACCTTGTCTGACGACG 506
OY 421 TTGGCTGCTGATGTGGCA--GGCGGCCAGCGTGAATTCATGCTGGGCGACTGTA 478
DB 507 TTGGCTGCTGATGTGGCAAGGCGCGCCAGCGTGAATTCATGCTGGGCGACTGTA 566
OY 479 TCATCAGATCTTCAAGCTGTAGGCGCTGAGGGGCTCTACGAGGTTCAACGCTCTG 538
DB 567 TCATCAGATCTTCAAGCTGTAGGCGCTGAGGGGCTCTACGAGGTTCAACGCTCTG 626
OY 539 TCAGAGCATATATATATAGAGTGGCTTCTGAGTGTATGATATCTGCAAGGGA 598
DB 627 TCAGAGCATATATATATAGAGTGGCTTCTGAGTGTATGATATCTGCAAGGGA 686
OY 599 TGTGCTGACCCCAAGACGTCACATTTTGTGACCTGTATGATGTCGCAAGTGTGA 658
DB 687 TGTGCTGACCCCAAGACGTCACATTTTGTGACCTGTATGATGTCGCAAGTGTGA 746
OY 659 CGGAGTGGCAGAGGCTGCTGTCTTACCCCTTGGACACTGTCGTGTAGATGATGTC 718
DB 747 CGGAGTGGCAGAGGCTGCTGTCTTACCCCTTGGACACTGTCGTGTAGATGATGTC 806
OY 719 AGTCCGCGCGGAAAGGCGCGCATATATATGTACAGCGGAGATTGACTGCTGA 772
DB 807 AGT-CGGCGGAAAGGCGCGCATATATATGTACAGCGGAGATTGACTGCTGA 859

RESULT 3
BM230491/c 1073 bp mRNA linear EST 31-JAN-2002
LOCUS K0296810-3 NIA Mouse unfertilized Egg cDNA Library (Long) Mus
DEFINITION Musculus cDNA clone K0296810 3', mRNA sequence.
ACCESSION BM230491
VERSION BM230491.1 GI:17793731
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1073)
Pisio,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Steag,C.A.,
Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(Long)
Unpublished (2001)
JOURNAL Laboratory of Genetics
COMMENT Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0296 row: B column: 10
Seq primer: -21M13 Forward
High quality sequence stop: 1073
POLYA-Yes.

FEATURES
Source Location/Qualifiers
1..1073
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:K0296810-3"
/db_xref="taxon:10090"
/clone="K0296810"
/clone_11b="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 1488 unfertilized eggs.

Double-stranded cDNAs were synthesized with an Oligo(dT)
primer [Invitrogen:
5'-pGACTAGTCTAGATCGGAGCGGCCCGCTTTTCTTTT-3'],
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA).
BASE COUNT 249 a 309 c 272 g 237 t 6 others
ORIGIN

Query Match 82.0%; Score 733.2; DB 13; Length 1073;
Best Local Similarity 89.9%; Pred. No. 31e-194;
Matches 807; Conservative 0; Mismatches 87; Indels 4; Gaps 2;
1 ATGGGTATCAAGCTTGGAGCTTCTTAAGACATTCCTGGCGGGCGGCGCTCC 60
DB 959 ATGGGGATCAAGCTTGGAGCTTCTTAAGACATTCCTGGCGGGCGGCGCTCC 900
OY 61 GTCT-CCAGACCGCGGTGCGCCCATGAGAGGCTCAAACTGCTGTGACAGTCCACA 119
DB 899 GTCTNCCAGACCGCGGTGCGCCCATGAGAGGCTCAAACTGCTGTGACAGTCCACA 840
OY 120 TGCCAGCAACAGATCACTGTGAGAGACATACAAAGGATCATTTGTTGTTGAG 179
DB 839 TGCCAGCAACAGATCACTGTGAGAGACATACAAAGGATCATTTGTTGTTGAG 780
OY 180 AATCCCTAAGAGAGAGCGCTTCTCTCTTGTGAGAGGCTTAACCTGGCGCAAGTATCCG 239
DB 779 AATCCNCCAGAGAGAGCGCTTCTCTCTTGTGAGAGGCTTAACCTGGCGCAAGTATCCG 720
OY 240 TTACTTCCCAACCCAGAGCTTCAACTTCCCTTGAAGAGCAAGTACAGACAGCTCTT 299
DB 719 GTACTTCCCAACCCAGAGCTTCAACTTCCCTTGAAGAGCAAGTACAGACAGCTCTT 660
OY 300 AGGGGTGTGATGGGCTAATAGACATTTGCGCTTCTGCTGTAACCTGGCGCTCCG 359
DB 659 GGAAGGCTGTGATGGGCTAATAGACATTTGCGCTTCTGCTGTAACCTGGCGCTCCG 600
OY 360 TGGGGCGCTGGGGCCACCTCCCTTGTGTGTACCCGCTGGACATTTGCTAGACCCAG 419
DB 599 TGGGGCGCTGGGGCCACCTCCCTTGTGTGTGTACCCGCTGGACATTTGCTAGACCCAG 540
OY 420 GTTGGCTGCTGATGTGGGCAAGGCG---CGCCAGCTGAGTTCATGCTGTGGGCACTG 476
DB 539 GCTGGCTGCGAGCGGGGCAAGGAGTGTCTCCACAGCAATTAATGAGCGCTGGGCACTG 480
OY 477 TATCATCAAGATTTCAAGTGTATGGCTGAGGGGCTCTACAGGCTTTCAACGCTCTC 536
DB 479 TCTCACCAAGATTTCAAGTGTATGGCTGAGGGGCTCTACAGGCTTTCAACGCTCTC 420
OY 537 TGTCCAGGCAATTTATCTATAGAGTGGCTTGTGGAGTCTATGATATGTCGCAAGGG 596
DB 419 TGTCCAGGCAATTTATCTATAGAGTGGCTTGTGGAGTCTATGATATGTCGCAAGGG 360
OY 597 GATGCTGCTGACCCCAAGACGTCACATTTTGTAGCTGATGATATGTCGCAAGGCT 656
DB 359 GATGCTGCTGACCCCAAGACGTCACATTTTGTAGCTGATGATATGTCGCAAGGCT 300
OY 657 GACGCAAGTGGCAGAGGCTGCTCTTACCCCTTGTGACATGCTGCTGATGATGAT 716
DB 299 GACGCAAGTGGCAGAGGCTGCTCTTACCCCTTGTGACATGCTGCTGATGATGAT 240
OY 717 GCAGTCCGCGCGGAAAGGCGCGATTTATGTATACAGGGGACACTTACTGCTGAGGAA 776
|||||

Dh 239 GCAGTGTGGCCGGAAAGGGGCTGATATATGTACAGGGGACATTGACTGTGAGGAA 180
Oy 777 GATTGCAAAAGACGAGAGAGCCAGAGCCTTCTTCAAGAGTGGCTGCTCAATGCTGAG 836
Dh 179 GATTGCAAAAGATGAGAGAGCCAGAGCCTTCTTCAAGAGGCTTGGCTCAATGCTGAG 120
Oy 837 AGGCATGCGGGGCTTTTGTATTTGGTGTGTATGATGATCAAAAATATGCTGAA 894
Dh 119 AGGCATGCGGTGGCTTTTGTATTTGGTGTGTATGATGATCAAAAATATGCTGAA 62

RESULT 4

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B1754652 925 bp mRNA linear EST 25-SEP-2001
603025339F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196080 5',
mRNA sequence.
B1754652
B1754652.1 GI:15746230
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 925)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM11490 row: m column: 09
High quality sequence stop: 791.
Location/Qualifiers
1. 925
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5196080"
/clone_1ib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCMV-SPORT6; Site: 1; Note: 1;
Site: 2; EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb. Insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH-MGC Library."

FEATURES

SOURCE

BASE COUNT 184 a 249 c 294 g 198 t
ORIGIN
Query Match 80.2%; Score 717.4; DB 13; Length 925;
Best Local Similarity 96.5%; Pred. No. 7.7e-190;
Matches 798; Conservative 0; Mismatches 21; Indels 8; Gaps 6;

Oy 1 ATGGGTGATCAGCCTTGAGACTTCTTAAAGACTTCTGCGCGGCGCTGCCCTGCC 60
Dh 98 ATGGGTGATCAGCCTTGAGACTTCTTAAAGACTTCTGCGCGGCGCTGCCCTGCC 157
Oy 61 GTCTCAAGACCGCGGCTGCGCCATCGAGAGGTCAAACTGCTGCTGACGATCAGCAT 120
Dh 158 GTCTCAAGACCGCGGCTGCGCCATCGAGAGGTCAAACTGCTGCTGACGATCAGCAT 217
Oy 121 GCCAGCAACAGATCACTGCTGAGAACAGCACTACAAAGCATTTGATGCTGTGAGCA 180
Dh 218 GCCAGCAACAGATCACTGCTGAGAACAGCACTACAAAGCATTTGATGCTGTGAGCA 277

Oy 181 ATCCCTAAGAGAGAGGCGTTCTCTCTCTCTCTGAGAGGCGTAACCTGGCCAAAGTCCT 240
Dh 278 ATCCCTAAGAGAGAGGCGTTCTCTCTCTCTCTGAGAGGCGTAACCTGGCCAAAGTCCT 337
Oy 241 TACTTCCCAACCAAGCTCTCAACTTCCGCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 300
Dh 338 TACTTCCCAACCAAGCTCTCAACTTCCGCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 397
Oy 301 GGGGCTGTGAGATGCGCATAGACAGTTCTGAGCGCTACTTTGCTGTGTAACCTGGCGTCCGT 360
Dh 398 GAGGCTGTGAGATGCGCATAGACAGTTCTGAGCGCTACTTTGCTGTGTAACCTGGCGTCCGT 457
Oy 361 GGGGCGGCTGAG 420
Dh 458 GGGGCGGCTGAG 517
Oy 421 TTGGCTGTGATGTGGCGAGGCG---CGGCCAGCTGAGTTCATGCTGCGGCGACTGT 477
Dh 518 TTGGCTGTGATGTGGCGAGGCGCGCGCCGACGCTGATGCTGCTGCTGCTGCTGCTG 577
Oy 478 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGCGCTTACAGAGTTTCAAGCTCTCT 537
Dh 578 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGCGCTTACAGAGTTTCAAGCTCTCT 637
Oy 538 GTCCAAAGCATCTATTCTATAGAGCTGCTTCTGAGAGCTATGATATCTGCCAAGGGG 597
Dh 638 GTCCAAAGCATCTATTCTATAGAGCTGCTTCTGAGAGCTATGATATCTGCCAAGGGG 697
Oy 598 ATGC-TGCCGAGCCCAAG-CAGAGCTCATATTTTGTGAGCTGAGATGATGCCAGAGTG 655
Dh 698 ATGCTTGGCTGAG 757
Oy 656 TGAGGAG 714
Dh 758 TGAGGAG 817
Oy 715 ATGCACTCCGCGCGGAG 774
Dh 818 ATGCACTCCGCGCGGAG 876
Oy 775 AGCATGCAAAAG 821
Dh 877 AGCATGCAAAAG 922

RESULT 5
LOCUS AL561542 909 bp mRNA linear EST 16-FEB-2001
DEFINITION AL561542 LTI_NFL010_BC2 Homo sapiens cDNA clone CSDBL011YJ23 5
ACCESSION AL561542 prime, mRNA sequence.
VERSION AL561542
KEYWORDS AL561542.1 GI:12909075
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 909)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.
Location/Qualifiers
1. 909
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDBL011YJ23"
/clone_1ib="LTI_NFL010_BC2"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"

FEATURES
SOURCE

/note="vector: pcwvSPORT 6; site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pcwvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetechn.com URL: http://fulllength.invitrogen.com"

BASE COUNT 183 a 237 c 287 g 198 t 4 others

ORIGIN

Query Match 80.1%; Score 715.8; DB 9; Length 909;
Best Local Similarity 96.5%; Pred. No. 2.2e-189;
Matches 793; Conservative 3; Mismatches 16; Indels 10; Gaps 6;

OY 1 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCCGCGCGCGCGCGCTGCC 60
DB 90 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCCGCGCGCGCGCGCTGCC 149
OY 61 GTCTCCAGAGCCGGGTGCGCCCATCGAG---AGGCTCAACTGCTGCTGACAGTCCA 116
DB 150 GTCTCCAGAGCCGGGTGCGCCCATCGAGAGGAGGAGGAGGAGGAGGAGGAGTCCA 209
OY 117 GCATGCCAGCAAGACAGTACGCTGAGAGCAGTACAAAGGAGTCAATGATGTGTGT 176
DB 210 GCATGCCAGCAAGACAGTACGCTGAGAGCAGTACAAAGGAGTCAATGATGTGTGT 269
OY 177 GAGAAATCCCTTAAGAGCAGGCGCTTCTCTTCTGAGAGGAGTAACTGGCCCAAGTAT 236
DB 270 GAGAAATCCCTTAAGAGCAGGCGCTTCTCTTCTGAGAGGAGTAACTGGCCCAAGTAT 329
OY 237 CCGTTACTTCCCAACCCAGCTCTCAACTGCTTCAAGAGCAAGTACAGACAGCTCTT 296
DB 330 CCGTTACTTCCCAACCCAGCTCTCAACTGCTTCAAGAGCAAGTACAGACAGCTCTT 389
OY 297 CTTAGGGGCTGATGCGCATGAGCAATCTGCGGCTACTTGTGTGTAACCTGCGCTC 356
DB 390 CTTAGGGGCTGATGCGCATGAGCAATCTGCGGCTACTTGTGTGTAACCTGCGCTC 449
OY 357 CCGTGGGCGCGCTGGGCGCACCTCCCTTGTCTTGTCTCAACCGCGGACTTGTCTAGAC 416
DB 450 CCGTGGGCGCGCTGGGCGCACCTCCCTTGTCTTGTCTCAACCGCGGACTTGTCTAGAC 509
OY 417 CAGTTGGCTCTGATGTGGCAGGCGCGC--CCAGCGTGAATTC-ATGCTTGGGCGCA 473
DB 510 CAGTTGGCTCTGATGTGGCAGGCGCGCCTGAGTTCATGCTGCTGGGCGCA 569
OY 474 CTTATATCATCAAGATCTTCAAGTCTGATGGGCTGAGGGGCTCTAACCAGGCTTTCACGT 533
DB 570 CTTATATCATCAAGATCTTCAAGTCTGATGGGCTGAGGGGCTCTAACCAGGCTTTCACGT 629
OY 534 CTCTGTCCAGGCAATCATTTATATAGAGTGCCTACTTGCAGCTCTTATAGTACGCCAA 593
DB 630 CTCTGTCCAA--GCATCATTTATCTATAGAGTGCCTACTTGCCTGCTCTATACGCCAA 688
OY 594 -GGGAGTCTCTGACCCCAAGAGCTGCACATTTTGTAGCTGATGATGGCCAGA 652
DB 689 GGGAGTCTCTGACCCCAAGAGCTGCACATTTTGTAGCTGATGATGGCCAGA 748
OY 653 GTGTGAGGCAAGTGGCAGGCGCTGCTACCCCTTGTAGACCTGCTGCTGTAAGAA 712
DB 749 GTGTGAGGCAAGTGGCAGGCGCTGCTACCCCTTGTAGACCTGCTGCTGTAAGAA 808
OY 713 TGATGCACTCCGCGGAGAAAGGCGCATTTATGTATACAGGGGAGCACTTACTGCTGA 772
DB 809 TGATGCACTCCGCGGAGAAAGGCGCATTTATGTATACAGGGGAGCACTTACTGCTGA 868
OY 773 GGAAGATTGCAAAAGAGAGAGCAAGGCGCTTCTTCAAG 814
DB 869 GGAAGATTGCAAAAGAGAGAGCAAGGCGCTTCTTCAAGG 909

RESULT 6
BM466452
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNL12143 row: 1 column: 16
High quality sequence stop: 744.
Location/Qualifiers

FEATURES
source

1..1043
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5503575"
/clone_id="NIH-MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcwv-SHORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

BASE COUNT 204 a 295 c 309 g 234 t 1 others

ORIGIN

Query Match 79.7%; Score 712.4; DB 13; Length 1043;
Best Local Similarity 97.8%; Pred. No. 2e-188;
Matches 744; Conservative 0; Mismatches 12; Indels 5; Gaps 2;

OY 1 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCCGCGCGCGCGCGCTGCC 60
DB 91 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCCGCGCGCGCGCGCTGCC 150
OY 61 GTCTCCAGAGCCGGGTGCGCCCATCGAGAGGAGTCAACTGCTGCTGACAGTCCAGAT 120
DB 151 GTCTCCAGAGCCGGGTGCGCCCATCGAGAGGAGTCAACTGCTGCTGACAGTCCAGAT 210
OY 121 GCCAGCAAGACATCAGTCTGAGAAACAGTACAAAGGAGTCAATGATGTGTGTAGA 180
DB 211 GCCAGCAAGACATCAGTCTGAGAAACAGTACAAAGGAGTCAATGATGTGTGTAGA 270
OY 181 ATCCCTAAGAGCAGGCGCTTCTCTCTTCTGAGAGGAGTAACTGGCCCAAGTATCGGT 240
DB 271 ATCCCTAAGAGCAGGCGCTTCTCTCTTCTGAGAGGAGTAACTGGCCCAAGTATCGGT 330
OY 241 TACTTCCCAAGCAGCTCTCACTTGCCTTCAAGAGCAAGTACAGAGCTCTTCTTA 300
DB 331 TACTTCCCAAGCAGCTCTCACTTGCCTTCAAGAGCAAGTACAGAGCTCTTCTTA 390
OY 301 GGGGCTGTGATCGCGCATTAAGCACTTCTGCGGCTCACTTGTGTATACCTGCGGCT 360
DB 391 GGGGCTGTGATCGCGCATTAAGCACTTCTGCGGCTCACTTGTGTATACCTGCGGCT 450
OY 361 GGGGCTGTGCGGCGCTCTCTTGTGTGTATACCTGCGGCTCACTTGTGTATACCTGCGG 420

Db 451 GGGGGCGGGGGCCACGCTTGTGCTTGTCTACCCGCTGACTTTGCTAGACAGG 510

Qy 421 TTGGCTGCTGATGTGGCAGAGCG---CGCCAGCGCTGAGTTCATGCTGTGGCGACTGT 477

Db 511 TTTGGCTGCTGATGTGGCAGAGCGCGCCGCGCAGCTGAGTTCATGCTGTGGCGACTGT 570

Qy 478 ATCATCAAGATCTTCAAGCTGTGATGGCGCTGAGAGGGGCTCTACAGAGTTTCAAGCTCTCT 537

Db 571 ATCATCAAGATCTTCAAGCTGTGATGGCGCTGAGAGGGGCTCTACAGAGTTTCAAGCTCTCT 630

Qy 538 GTCCAAAGGATCATTTATCTATAGAGCTGCTACTTCTGAGATCTATGATTAAGTCCAGAGG 597

Db 631 GTCCAAAGGATCATTTATCTATAGAGCTGCTACTTCTGAGATCTATGATTAAGTCCAGAGG 690

Qy 598 ATGCTGCTGACCCCAAGAACCTGCACATTTTGTGAGCTGTGATTTGCCAGAGTGTG 657

Db 691 ATGCTGCTGACCCCAAGAACCTGCACATTTTGTGAGCTGTGATTTGCCAGAGTGTG 750

Qy 658 AGGAGATGCGAGGGCTGCTGTCTACCCCTTGTGACACTGTCTGTAGATGATGATGATG 717

Db 751 AGGAGATGCGAGGGCTGCTGTCTACCCCTTGTGACACTGTCTGTAGATGATGATGATG 810

Qy 718 CAGTCCGCGCGG--AAAGGGCCGATATTATGTACAGCGGG 756

Db 811 CAGTCCGCGCGCGAAGAGGCGCCCATATTATGTACCGCGG 851

RESULT 7 990 bp mRNA linear EST 05-SEP-2001
LOCUS B1545249 603187373f1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5258778 5',
DEFINITION mRNA sequence.

ACCESSION B1545249
VERSION B1545249.1 GI:15432561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE NIH-MGC
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM11652 row: a column: 19
High quality sequence stop: 760.

FEATURES
source Location/Qualifiers
1..990

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258778"
/clone_lib="NIH_MGC_95"
/issue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
size-selected for average insert size 2.5 kb and
normalized to ROP 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT

191 a 262 c 320 g 217 t

ORIGIN

Query Match 79.4%; Score 709.6; DB 13; Length 990;
Best Local Similarity 93.4%; Pred. No. 1.2e-187;
Matches 818; Conservative 0; Mismatches 49; Indels 9; Gaps 7;

Qy 1 ATGGGTGATTCACGCTTGAGAGCTTCCTTAAGAGACTTCGCGCGGGGGCTGCGCGCTCC 60

Db 113 ATGGGTGATTCACGCTTGAGAGCTTCCTTAAGAGACTTCGCGCGGGGGCTGCGCGCTCC 172

Qy 61 GTCTCCAGAGACCGCGGTGCGCCCATTCGAGAGAGGCTCAAACTGCTCTGCTCAGGTCCAGCAT 120

Db 173 GTCTCCAGAGACCGCGGTGCGCCCATTCGAGAGAGGCTCAAACTGCTCTGCTCAGGTCCAGCAT 232

Qy 121 GCCAGCAAGAGATCAGTGTGAGAGAGAGTCAAGAGGATCATTTGATGTTGCTGTAGA 180

Db 223 GCCAGCAAGAGATCAGTGTGAGAGAGAGTCAAGAGGATCATTTGATGTTGCTGTAGA 292

Qy 181 ATCCCTAAGAGAGAGGCTTCT 240

Db 293 ATCCCTAAGAGAGAGGCTTCT 352

Qy 241 TACTTCCCCACCCAGCTCTCAACTTCCCTTCAAGAGACAGTACAGACAGCTTCTTCTTA 300

Db 353 TACTTCCCCACCCAGCTCTCAACTTCCCTTCAAGAGACAGTACAGACAGCTTCTTCTTA 412

Qy 301 GGGGCTGTGATCGGCATTAAGAGACTTCTGCGGCTACTTCTGCTGTTACCTGCGTCCGT 360

Db 413 GGGGCTGTGATCGGCATTAAGAGACTTCTGCGGCTACTTCTGCTGTTACCTGCGTCCGT 472

Qy 361 GGGGCTGTGAGGCGCACCTCCCTTGTGCTTGTGCTACCGCGCTGAGTCTGTGAGACAGG 420

Db 473 GGGGCTGTGAGGCGCACCTCCCTTGTGCTTGTGCTACCGCGCTGAGTCTGTGAGACAGG 532

Qy 421 TTGGCTGCTGATGTGGCAGAGC--CGCCAGACGCTGAGTTCATGCTGTGGCGACTGTA 478

Db 533 TTGGCTGCTGATGTGGCAGAGCGCGCCGCGCAGCGTGCATGCTGTGGCGACTGTA 592

Qy 479 TCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGCGCTCTACAGAGGTTTCAAGCTCTCTG 538

Db 593 TCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGCGCTCTACAGAGGTTTCAAGCTCTCTG 652

Qy 539 TCCAA-GGCATCATTAATCTATAGAGCTGCTGAGTCTGAGTCTATGATTAAGTCCAGAGG 597

Db 653 TCCAAAGGATCATTAATCTATAGAGCTGCTGAGTCTGAGTCTATGATTAAGTCCAGAGG 712

Qy 598 ATGCTGCTGTA-CCCAAGAGAGCTGACATTTTGTG-AGCTGATGATTTGCCAGAGTG 655

Db 713 ATGCTGCTGAGAGCCCAAGAGAGCTGCCATTTTGTGAGAGCTGATGATTTGCCAGAGTG 772

Qy 656 TGACGGCAGTGCAGAGGCTCTG-TCTAACCCCTTTCACACTGTTCTGCTAGATGATG 714

Db 773 TGACGGCAGTGCAGAGGCTCTG-TCTAACCCCTTTCACACTGTTCTGCTAGATGATG 832

Qy 715 ATGCAGTCCGCGCGAAGAGGCGCATTTATGTACAGAGGGA-CAGTTGACTGTGAG 773

Db 833 ATTCATCCGCGCGAAGAGGCGCGAATTTATGTACAGAGGAGCAGGCTGCTGAG 892

Qy 774 GAGATTTCCAAAG 833

Db 893 GAGATTTCCAAAG 950

Qy 834 GAGAGCATGGCGGCTGCTTTTGTATTTGCTGTTGTA 869

Db 951 GAGAGCATGGCGGCTGCTTTTGTATTTGCTGTTGTA 986

RESULT 8 1033 bp mRNA linear EST 14-AUG-2001
LOCUS B1408731 602965692f1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5121071 5',
DEFINITION mRNA sequence.
ACCESSION B1408731

VERSION	BI408731.1	GI:15169654
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1033)	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D.	

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonafido, Ph.D.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
plate: LLAM1295 row: 9 column: 24
High quality sequence start: 5
High quality sequence stop: 917.

FEATURES
SOURCE

Location/Qualifiers
1. .1033

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/organism="Mus musculus"
/strain="CZECH 11"
/db_xref="taxon:10090"
/clone_image="5121071"
/clone_id="NC1.CGAP.Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DJ10B (phage-resistant)"
/notes="Organ: Lung: Vector: pPT30-Pac (Pharmacia) with a
modified polylinker. Site_1: NotI. Site_2: EcoRI. 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5].
TGTTCACATCTGAAAGGCGCGCCGCTCTGTTTTTTTTTTT 3' ].
(Poolable-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the NotI
I and Eco RI sites of the modified pT733 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
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BASE COUNT
CRIGIN

217 a 267 c 310 g 239 e

Query Match	78.0%;	Score 697.2;	DB 13;	Length 1033;
Best Local Similarity	88.0%;	Pred. No. 3.7e-184;		
Matches 783; Conservative	0;	Mismatches 103;	Indels 4;	Gaps 2;

QY 1 ATGGGGAATCAGCGTTTGGAGCTTCCTTAAGAAGATTCTCGCCGGGGGGCGTGCGCGTGC 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 76 ATGGGGGATCAGCGTTTGAAGCTTTCTTAAGGACTTCTTGCAAGTGGCATGCGCGCGCG 139
QY 61 GTCTCCAACGCCGGGTGSCCCCCATTCGAAGAGGGTAAACTGCTGCTGCAGATCCACAT 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 136 GTCTCCAACGCCGGGTGSCCCCCGATTCGAAGAGGGTAAACTGCTGCTGCAGATCCACAT 195
QY 121 GCCAGCAAAACAGATCAGTCTGCTGAAGACAGTACAAGGATCATTTGATTGCTGTGAGA 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 196 GCGACAAACAGATCATGTCGACAGAAAGACAGTACAAAAGCATCTATTGTTGTGTGTGAGA 255
QY 181 ATTCCTTAAGGAGCAGGGCTTCTCTCTCTTGTGAGGGGTAACTGGCCAACGTGATCCGT 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 256 ATTCCTTAAGGAGCAGGGCTTCTCTCTCTTGTGAGGGGTAACTGGCCAACGTGATCCGT 315
QY 241 TACTTCCCACCAAGCTCTCAACTTCGCTTAAAGACAAAGTACAAGCAGCTCTTCTTA 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 316 TACTTCCCACCAAGCTCTCAACTTCGCTTCAAAGACAAAGTACAAGCAGCTCTTCTCTG 375
QY 301 GGGGGGTGGATGGGATTAAGCAGTCTGGCGCTACTTTCCTGTAAACGCGGGGCTCCGT 360
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 376 GGAGGCGGTGATGCGCATTAAGCAGTCTGGCGCTACTTTCCTGTAAACGCGGGCTCTGAT 435

421 TTGGCTGCTGATGTTGGGACGGG---CGCCACGCTGAGTTCATGCTCTGGGCGACTGT 477
 496 CTGGCTGGCGAAGTGGGGACAGGGAGATCTTCCAGCGAGAAATTCATATGGCGCTGGGCGACTGT 555
 478 ATCATCAGAGATCTTCAAGTCTGATGGCCCTGAGGGGGCTTACCAGGGTTTCAACGTCCT 537
 556 CTCACCAAGATCTTCAAGTCGGACGGCCCTGAAGGGGTCTTACACGAGGTTTCAATGTCCT 615
 538 GTCCAGAGCATCATATATCTATAGAGCTGCTACTTGGGAGCTATATATCTGCGAAGGG 597
 616 GTCCAGGGCATATCATCTACAGAGCTGCTACTTGGGAGTCTATATACACTGCGCAAGGG 675
 598 ATCGACGCCGACCCCAAGACGTGCACATTTTGTAGAGTGGATGATGGCCAGAGTGT 657
 676 ATGCTGCCAGACCCCAAGAGATGTGCACATTATGCTGAGCTGATGATTTGCCACAGATGT 735
 658 ACGGAGATCG--CAGGGCTGCTGCTCAACCCCTTTGACACTGTTCGTTGTAATGATGAT 716
 736 ACAGCGGTGGCCGGGGCTGTGTCTCAATCCGTTTGACACTGTTCGTTGTAATGATGAT 799

Qy	717	CGAGTCGGCCCGAAAGGGCCGATTTTATGTACACGGGGACAGTTGACTGCTGGAGGAA	776
Db	766	CGAGTCGGCCCGAAAGGGCGCTGATATTATGTACACGGGGACACTTGACTGCTGGAGGAA	855
Qy	777	CATTGCCAAAGACGAAGAGCCCAAGCCCTTCTTCAAAAGTCCTGCTCCAAATGCTGGAG	836
Db	856	CATTGCCCAAGATGAAGAGCCCAACCCTTTCTTCAAAAGGCGCTTGGTCCCAATGTACTGAG	915
Qy	837	AGCCATGGCGCGCTCTTTTGTATTGGTGTGTTGATGATGACATCAAAAAT	886
Db	916	AGCGCTTGGCGTGTCTCTTGATGGCGCATGATTTGAATGAGATCACCAACT	965

RESULT 9	
B1458368	
LOCUS	B1458368 879 bp mRNA linear EST_21-AUG-2001
DEFINITION	603198738T1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5278233 5' , _
ACCESSION	mRNA Sequence.
VERSION	B1458368 B1458368.1 GI:15249024

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 879)	Emmerylo; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NIH-MGC	http://mgc.ncl.nih.gov/			
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgabds@email.nih.gov				
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.				
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroaki Toshiyuki and Piero Carninci (RIKEN)				
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
Plate: LLAM1702	row: 1	column: 10		
High quality sequence step: 776.				

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location/Qualifiers
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/db_xref="taxon:9606"
/clone IMAGE:5278233
/clone_1lb="NH_MCC-96"
/tissue_type="hypothalamus"
/lab_host="DH10b"
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/note="Organ: brain; Vector: PbluescriptR (modified pbluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcga)
) : Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTAA-3',
size selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."
BASE COUNT 175 a 234 c 267 g 203 t
ORIGIN

Query Match 76.2%: Score 681.2: DB 13: Length 879:
Best Local Similarity 96.5%: Pred. No. 1e-179:
Matches 762: Conservative 0: Mismatches 18: Indels 10: Gaps 6:

OY 1 ATGGGTCATCAGCTTGGAGCTTCTAAAGAGCTCTCGCGCGGCGTCCGCGTCC 60
DB 60 ATGAGTATCAGCTTGGAGCTTCTAAAGAGCTCTCGCGCGGCGTCCGCGTCC 119
OY 61 GTCTCCAAAGACCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCC 120
DB 120 GTCTCCAAAGACCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCC 179
OY 121 GCCAGCAAGAGATCAGTCTGAGAGAGAGTACAAAGGAGTATGCTGCTGAG 180
DB 180 GC---CAACACATCACTGCTGAGAACACTACAAAGAGATGATGCTGAG 236
OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 237 ATCCCTAAGAGAGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 296
OY 241 TACTTCCGCGCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGT 300
DB 297 TACTTCCGCGCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCCGCGT 356
OY 301 GGGGCTGCTGAGTGGGCTAAGAGAGTCTGCGCTCTCTCTCTCTCTCTCTCT 360
DB 357 GGGGCTGCTGAGTGGGCTAAGAGAGTCTGCGCTCTCTCTCTCTCTCTCTCT 416
OY 361 GGGGCTGCTGAGTGGGCTAAGAGAGTCTGCGCTCTCTCTCTCTCTCTCTCT 420
DB 417 GGGGCTGCTGAGTGGGCTAAGAGAGTCTGCGCTCTCTCTCTCTCTCTCTCT 476
OY 421 TTGGCTGCTGAGTGGGCTAAGAGAGTCTGCGCTCTCTCTCTCTCTCTCTCT 477
DB 477 TTGGCTGCTGAGTGGGCTAAGAGAGTCTGCGCTCTCTCTCTCTCTCTCTCT 536
OY 478 ATCATCAAGATCTTCAAGTCTGAGTGGGCTGAGGAGGCTTCAAGAGTCTCT 537
DB 537 ATCATCAAGATCTTCAAGTCTGAGTGGGCTGAGGAGGCTTCAAGAGTCTCT 596
OY 538 GTCCAAGAGATCTTCAAGTCTGAGTGGGCTGAGGAGGCTTCAAGAGTCTCT 596
DB 597 GTCCAAGAGATCTTCAAGTCTGAGTGGGCTGAGGAGGCTTCAAGAGTCTCT 656
OY 597 GATGCTGCTGAGTGGGCTAAGAGAGTCTGAGTGGGCTGAGTGGGCTGAGT 655
DB 657 GATGCTGCTGAGTGGGCTAAGAGAGTCTGAGTGGGCTGAGTGGGCTGAGT 716
OY 656 TGACGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTG 715
DB 717 TGACGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTG 775
OY 716 TGACGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTG 775
DB 776 TGACGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTG 834
OY 776 AGATTCGCAA 785
DB 835 AGATTCGCAA 844

RESULT 10
LOCUS BM459526 882 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6417828 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534143
5', mRNA sequence.
ACCESSION BM459526
VERSION BM459526.1 GI:18508566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 882)
REFERENCE NIH-MGC <http://mgc.ncl.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cga@fremail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12220 row: c column: 08
high quality sequence stop: 731.
Location/Qualifiers
1. 882

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5534143"
/clone_lib="NIH_MGC_71"
/issue_type="telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pcwv-SPO6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 204 a 208 c 241 g 229 t
ORIGIN

Query Match 75.7%: Score 676.6: DB 13: Length 882:
Best Local Similarity 99.0%: Pred. No. 2e-178:
Matches 692: Conservative 0: Mismatches 4: Indels 3: Gaps 1:
OY 199 TTCT 258
DB 2 TTCT 61
OY 259 CTCACTTCT 318
DB 62 CTCACTTCT 121
OY 319 AACGATTTGGGCTGAGTGGTCTGTAACCTGCGCGGCGGCGGCGGCGGCGG 378
DB 122 AACGATTTGGGCTGAGTGGTCTGTAACCTGCGCGGCGGCGGCGGCGGCGG 181
OY 379 TCCCTTTCT 438
DB 182 TCCCTTTCT 241
OY 439 AGGCG---CGGCCAGGCTGAGTGGTCTGTAACCTGCGCGGCGGCGGCGG 495
DB 242 AAGGCGCGCGCGCGAGTGGTCTGTAACCTGCGCGGCGGCGGCGGCGGCGG 301
OY 496 TCTGATGCGCTGAGGCGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTATC 555
DB 302 TCTGATGCGCTGAGGCGCTTCAAGAGGCTTCAAGAGGCTTCTCTCTCTCTATC 361
OY 556 TATAGAGTCT 615
DB 362 TATAGAGTCT 421

QY	616	AACGTGCACATTTTGTGAGCTGGATGATTTGCCAGATGTGACGGGACGTGCAGAGCGTG	675
Db	422	AACGTGCACATTTTGTGAGCTGGATGATTTGCCAGATGTGACGGGACGTGCAGAGCGTG	481
QY	676	CTGTCTTACCCCTTTGACACTGTTCTGCTGATGAATGATGATGCATCCGGCGGAAAGG	735
Db	482	GTGTCTTACCCCTTTGACACTGTTCTGCTGATGAATGATGATGCATCCGGCGGAAAGG	541
QY	736	GCCCATTTATGTACACGGGGACAGTTGACTGTGGAGAGAGATTGCCAAAGACAGACGA	795
Db	542	GCCCATTTATGTACACGGGGACAGTTGACTGTGGAGAGAGATTGCCAAAGACAGACGA	601
QY	796	GCCAAAGCCCTTCTTCAAAGGTGCCCTGATGCATATGTCTGAGAGGCATGGCGGCTCTTT	855
Db	602	GCCAAAGCCCTTCTTCAAAGGTGCCCTGATGCATATGTCTGAGAGGCATGGCGGCTCTTT	661
QY	856	GTAATGTCTCTATGATGAGATGCAAAAATAATGTCTTAA	894
Db	662	GTAATGTCTCTATGATGAGATGCAAAAATAATGTCTTAA	700

RESULT 11
B1667026
LOCUS B1667026 907 bp mRNA linear EST_12-SEP-2001
DEFINITION 603291895F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5311319 5',
mRNA sequence.
ACCESSION B1667026
VERSION B1667026
KEYWORDS GI:15581259
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 907)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999).
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1788 row: n column: 24
High quality sequence stop: 805.

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FEATURES
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Location/Qualifiers
1. 907
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:531319"
/clone_1lb="NIH_MCC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/Note="Organ: Brain; Vector: pBluescriptR (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTN-3',
size-selected for average insert size 2.3 kb and
normalized to RQ7 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carlnici, In preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MCC Library."
BASE COUNT
174 a 253 c 287 g 193 t
ORIGIN

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Query Match	75.0%;	Score 670.4;	DB 13;	Length 907;
Best Local Similarity	97.1%;	Pred. No. 1.1e-176;		
Matches 726; Conservative	0;	Mismatches 16;	Indels 6;	Gaps 4

Oy	1	ATGGGTGATACACGCTTGTGGAGCTTCTCTTAAGGACATTCCTGGCGGGGGGGGTTGGCCGCTGCC	60
Db	113	ATGGGTGTATCAGCGTTTGGAGCTTCTCTTAAGGACATTCCTGGCGGGGGGGGTTGGCCGCTGCC	172
Oy	61	GTCATCAAGACCGCGGTGGCCCATCATGAGAGGCTCAAACTGCTGTGCAGGTCCAGCAT	120
Db	173	GTCATCAAGACCGCGGTGGCCCATCATGAGAGGCTCAAACTGCTGTGCAGGTCCAGCAT	232
Oy	121	GCCAGCAAAACAGATCAGTGTGTGAGAAAGCAGTACAAAGGATCATTTGATTGTGTGTGAGA	180
Db	233	GCCAGCAAAACAGATCAGTGTGTGAGAAAGCAGTACAAAGGATCATTTGATTGTGTGTGAGA	292
Oy	181	ATCCCTAAGAGACAGGCGCTTCTCTCTCTTGTGAGAGGGGTAAOCTGGCCAAAGTATCCGT	240
Db	293	ATCCCTAAGAGACAGGCGCTTCTCTCTCTTGTGAGAGGGGTAAOCTGGCCAAAGTATCCGT	352
Oy	241	TACTTCCCCACCAAGCTCTCAACTTCCCTTTCAGAGACAGTACAAACAGCTCTTCTTA	300
Db	353	TACTTCCCCACCAAGCTCTCAACTTCCCTTTCAGAGACAGTACAAACAGCTCTTCTTA	412
Oy	301	GGGGGTGTGGATCGGCATTAAGCAGTTCGTGGCGCTACTTTGCTGTAACTTGCGCTCCGCT	360
Db	413	GGGGGTGTGGATCGGCATTAAGCAGTTCGTGGCGCTACTTTGCTGTAACTTGCGCTCCGCT	472
Oy	361	GGGGCGCGGTGGGGGCCACTCCCTTTGCTTTGCTATCCGCGGTGAGATTGGTGAAGACAGG	420
Db	473	GGGGCGCGGTGGGGGCCACTCCCTTTGCTTTGCTATCCGCGGTGAGATTGGTGAAGACAGG	532
Oy	421	TTCGGCTGATGTGGGACAGGCG--CGCCACGCTGAGTTCCATGCTGTGGCGACTGT	477
Db	533	TTCGGCTGATGTGGGACAGGCGCGCCCGCCAGCGCTGAGTTCCATGCTGTGGCGACTGT	592
Oy	478	ATCATCAAGATCTTCAAGTCTGATGAGGCGTGAAGGGGCTCTACAGAGGTTTCAACGCTCTCT	537
Db	593	ATCATCAAGATCTTCAAGTCTGATGAGGCGTCTGAGGGGCTCTACAGAGGTTTCAACGCTCTCT	652
Oy	538	GTCCAAAGCATATATTATCTATGAGCTGCTACTTCCGAGAGCTATGATATACGCAAGAGG	597
Db	653	GTCCAAAGCATATATTATCTATGAGCTGCTACTTCCGAGAGCTATGATATACGCAAGAGG	712
Oy	598	ATGCTGCGCAGCCCAAGACAGCTGCACATTTTGTGTGAGCT--GGATGATTGGCCACAGTGT	656
Db	713	ATGCTGCGCGA--CCCAAGACGTGCACATTTTGTGAGCTGGAGATGATTGGCCACAGTGT	771
Oy	657	GACGCGAGTGCAGGGCT--GCTGTCTTACCCCTTTGACACTGTTGCTGTAGATGATGA	715
Db	772	GACGCGAGTGCAGGGCTGTGGTGTCTTACCCCTTTTGACACTGTTGCGCGTAAAGTGTGA	831
Oy	716	TGCAGTCCGCGGGAAGGGCGCGATT 743	
Db	832	TGCCTGCGCGGCGGAAGGGCGCATAT 859	

RESULT	12
B0214399	
LOCUS	
DEFINITION	
ACCESSION	B0214399
VERSION	B0214398
KEYWORDS	B0214399.1 GI:20395799 EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia: Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 862)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: DCTD/BTP/Gazdar CDNA Library Preparation: Life Technologies, Inc.

0Y	241	TACTTCCCACCCAAAGCTCTCACTTGGCTTCAAGACAAAGTACAGACAGCTCTTTCTTAA	300
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0Y	301	GGGGGTGGAAATGGGCATTAAGAGATTTGGGGCTACTTGTGCTGTAACCTGGCCGCCGT	360
Db	362	GGAGGCGTGGATCGGCATTAAGAGATTTGGGGCTACTTGTGCTGTAACCTGGCCCTGCT	421
0Y	361	GGGGCGCGTGGGGCCACCTCCCTTTGCTTTGTCTACCGCGTGGACTTTGCTGAGAACAG	420
Db	422	GGGGGAGCTGGGGGCCACTCCCTCGCTTCGCTACACCGCGTGGACTTTGCTGAGAACAG	481
0Y	421	TTGGCTGCTGATGTGGGAGCGG--CGCCCAAGCGCTGATTCATAGTCTGGGCGACTGT	477
Db	482	CTGGCTGCGAGAGTGGGCAAGGAGATCTTCCGAGAGATTAATAGGCGCTGGCGACTGT	541
0Y	478	ATCATCAGATCTTCAAGTCTGATGGGCTGAGGGGGGCTCTACCAAGGTTTCAAGCTCT	537
Db	542	CTCACCAAGATCTTCAAGTCTGGAGCGGCTGGAAGGGTCTCTACCAAGGTTTCAAGTCTCT	601
0Y	538	GTCACAGACATCATATATATATAGAGACTGCTACTTGGGAGTGTATGATATCCCAAGGGG	597
Db	602	GTCACAGGACATCATATATCTACAGAGACTGCTACTTGGGAGTGTATGATACACTCCCAAGGGG	661
0Y	598	ATGCTGCTGAACCCCAAGAACGCTGCACATTTTGTAGACTGGATGATTGCCCAAGGTGTG	657
Db	662	ATGCTGCGACAGCCCAAGAAATGTGCACATTTATCGAGACTGGATGATGCCCAAGGTGTG	721
0Y	658	ACGGCAGTTCGACGGGCTGCTGTCTTACCCCTTTGACACTGTTCCGTCTGTAATGATGATG	717
Db	722	ACAGCGGTGGGGGGCTGTGTCTCATCCGTTTGCACCTGTTCTGTAAGATGATGATG	781
0Y	718	CAGTTCGGCGGAAAGGGGCGGATTTATGTAACAGGGGAGACTGTGCTGAGGAAG	777
Db	782	CAGTCTGGCGGAAAGGGGCTGATTTATGTAACAGGGGAGACTGTGCTGAGGAAG	841
0Y	778	ATTGCAAAAGACGAAGACCAAGGCTTTCTTCAAG	814
Db	842	ATTGC--AAAGATGAACGAGCAAGCCTTCTTCAAG	877

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RESULT 14
BI256359
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN1 at:
http://image.llnl.gov
Plate: LLM11278 row: k column: 06
High quality sequence stop: 789.
location/Qualifiers
1..948

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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone="IMAGE:5114621"
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/cclone_lib="NH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/notes="Organ: cervix; Vector: PCWV-SPOF6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.4 kb. Library prepared by 11ife
Technologies."
BASE COUNT      193 a      233 c      315 g      207 t
ORIGIN

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Oy	1	ATGGGTGATTCACGGCTTGGAGCCTTCTTAAAGGACATTCCTGGCCGGGGGGGGTGGCCGGCTGCC	60
Oy	96	ATGGGTGATTCACGGCTTGGAGCCTTCTTAAAGGACATTCCTGGCCGGGGGGGGTGGCCGGCTGCC	155
Oy	61	GTCTCCAAAGACCCGGCGTGCGCCCATCGAGAGGGTCAAACTGCTGTGCAGAGTCCACCAT	120
Db	156	GTCTCCAAAGACCCGGCGTGCGCCCATCGAGAGGGTCAAACTGCTGTGCAGAGTCCACCAT	215
Oy	121	GCACGCAAAACAGTACAGTGCCTGACACAGCAGTACAAAGGATCATTTGATTTGTGTGTGACA	180
Db	216	GCACGCAAAACAGTACAGTGCCTGACACAGCAGTACAAAGGATCATTTGATTTGTGTGTGACA	275
Oy	181	ATCCCTTAAGAGACAGGGCTTCTCTGCTCTTGGAGGGGTAACTGGCCCAACGTGATCCGT	240
Db	276	ATCCCTTAAGAGACAGGGCTTCTCTGCTCTTGGAGGGGTAACTGGCCCAACGTGATCCGT	335
Oy	241	TACTTCCCAACCCCAAGCTCTCACTTGCCTTTCAGGACACAGTACAGACAGCTTCTTCA	300
Db	336	TACTTCCCAACCCCAAGCTCTCACTTGCCTTTCAGGACACAGTACAGACAGCTTCTTCA	395
Oy	301	GGGGGTGTGATTCGGCATTAACAGCACTTCTGGGGCTACTTTGTGTAACTGTGGCTCCGGT	360
Db	396	GGGGGTGTGATTCGGCATTAACAGCACTTCTGGGGCTACTTTGTGTAACTGTGGCTCCGGT	455
Oy	361	GGGGCCGGTGGGGGACACCTCCCTTGGCTTTCCTACCCGGCTGAGACTTGGTAGAGACCAGG	420
Db	456	GGGGCCGGTGGGGGACACCTCCCTTGGCTTTCCTACCCGGCTGAGACTTGGTAGAGACCAGG	514
Oy	421	TTGGCTGCTGATGTGGGCAAGCG--GCCCCAGCGTAGTTCATGTGCTGGGCGCATGT	477
Db	515	TTGGCTGCTGATGTGGGCAAGCGCGCCCGCAGCGTAGTTCATGTGCTGGGCGCATGT	574
Oy	478	ATCATATCAAGATCTTCAAGTCTGATGTGGCTGAGGGGGCTTACCAAGGTTTCAACGTCCT	537
Db	575	ATCATATCAAGATCTTCAAGTCTGATGTGGCTGAGGGGGCTTACCAAGGTTTCAACGTCCT	634
Oy	538	GTCCAAGGCATCATTTATCTATAGAGCTGAGCTTCCGAGCTCTATGATTTACTGTCCAAAGGG	597
Db	635	GTCCAAGGCATCATTTATCTATAGAGCTGAGCTTCCGAGCTCTATGATTTACTGTCCAAAGGG	693
Oy	598	ATGCTGCTCAGCCCCCAAGAACGT-GCACATTTTTTGTGAGCTGATGATTTGCCCA----G	651
Db	694	ATGCTGCTCAGCCCCCAAGAACGTGSCACATTTTTTGTGAGCTGATGATTTGCCCAAGATT	753
Oy	652	AGTGTGAGGAGAGTGCAGAGGCTGTCTTACCCTTTTACACTGTGTCTCTTAAAGT	711
Db	754	AGTGTGAGGAGAGTGCAGAGGCTGTCTTACCCTTTTACACTGTGTCTCTTAAAGT	813
Oy	712	ATGATGTGAGTCCCGCGGAAAGGGGCGGATATTATGTATACAGGGGACAG-TTGACTGTCT	770
Db	814	ATGATGTGAGTCCCGCGGAAAGGGGCGGATATTATGTATACAGGGGACAGTGTAAATGTGT	873
Oy	771	GAGAGAGATTGCAAAAGACGAGAGGCCAAG	801
Db	874	GAGAGAGATTGCAAAAGACGAGAGGCCAAG	904

RESULT 15
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